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(54) **ANTI-ERBB3 ANTIBODIES AND USES THEREOF**

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(58) **Field of Classification Search**

None
See application file for complete search history.

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(57) **ABSTRACT**

The present invention provides antibodies that bind to ErbB3 and methods of using same. According to certain embodiments of the invention, the antibodies are fully human antibodies that bind to human ErbB3. In certain embodiments, the antibodies of the present invention block the interaction of ErbB3 with an ErbB3 ligand such as neuregulin 1. The antibodies of the invention are useful for the treatment of various cancers.

12 Claims, No Drawings

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ANTI-ERBB3 ANTIBODIES AND USES THEREOF

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a continuation of U.S. application Ser. No. 14/308,527, filed Jun. 18, 2014, now U.S. Pat. No. 9,284,380, which is a division of U.S. application Ser. No. 13/623,885, filed Sep. 21, 2012, now U.S. Pat. No. 8,791,244, which claims the benefit under 35 U.S.C. §119(e) of U.S. provisional application Nos. 61/541,312, filed on Sep. 30, 2011; 61/557,460, filed on Nov. 9, 2011; and 61/614,565, filed on Mar. 23, 2012, the disclosures of which are herein incorporated by reference in their entireties.

REFERENCE TO A SEQUENCE LISTING

This application includes an electronic sequence listing in a file named "474928-Sequence.txt", created on Feb. 1, 2016 and containing 183,991 bytes, which is hereby incorporated by reference in its entirety for all purposes.

FIELD OF THE INVENTION

The present invention relates to antibodies, and antigen-binding fragments thereof, which are specific for human ErbB3.

BACKGROUND

ErbB3 (also known as HER3) is a member of the ErbB/HER family of receptor tyrosine kinases (RTKs). Other members of this family include EGFR (also known as ErbB1 or HER1), ErbB2 (also known as HER2 or Neu), and HER4. ErbB receptors regulate cell proliferation, survival and differentiation by activating intracellular signaling cascades that lead to alterations in gene expression.

ErbB receptors are activated by the formation of either homo- or heterodimers. For example, when ErbB3 is co-expressed with ErbB2, an active heterodimeric signaling complex is formed. ErbB3 dimer formation is promoted by its ligand binding. Neuregulin 1 (NRG1) is the primary ligand for ErbB3 that promotes homo- or heterodimerization of the receptor.

ErbB3 has been found to be overexpressed in various cancer types, including breast, gastrointestinal, and pancreatic cancers. Anti-ErbB3 antibodies have been shown to inhibit the growth of several human tumor cell lines in mouse xenografts models. Anti-ErbB3 antibodies are mentioned in, e.g., U.S. Pat. Nos. 5,480,968; 5,968,511; US 2004/0197332; U.S. Pat. Nos. 7,332,580; 7,705,130; and 7,846,440. Nonetheless, there is a need in the art for novel ErbB3 antagonists, such as anti-ErbB3 antibodies, for the treatment of cancer and other related disorders.

BRIEF SUMMARY OF THE INVENTION

The present invention provides antibodies that bind human ErbB3. The antibodies of the invention are useful, inter alia, for inhibiting ErbB3-mediated signaling and for treating diseases and disorders caused by or related to ErbB3 activity and/or signaling.

The antibodies of the present invention, according to certain embodiments, block the interaction between ErbB3 and an ErbB3 ligand (e.g., NRG1 and/or NRG2). The antibodies may also possess one or more additional biologi-

cal properties such as, e.g., inducing cell surface ErbB3 internalization, inhibiting NRG1-stimulated tumor growth in vitro, and/or inhibiting tumor growth in vivo.

The antibodies of the invention can be full-length (for example, an IgG1 or IgG4 antibody) or may comprise only an antigen-binding portion (for example, a Fab, F(ab')₂ or scFv fragment), and may be modified to affect functionality, e.g., to eliminate residual effector functions (Reddy et al., 2000, J. Immunol. 164:1925-1933).

The present invention provides an antibody or antigen-binding fragment of an antibody comprising a heavy chain variable region (HCVR) having an amino acid sequence selected from the group consisting of SEQ ID NO: 2, 18, 34, 50, 66, 82, 98, 114, 130, 146, 162, 178, 194, 210, 226, 242, 258, 274, 290, 306, 322, 338, 354, 370, 386, 402, 418, 434, 450, 466 and 482, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

The present invention also provides an antibody or antigen-binding fragment of an antibody comprising a light chain variable region (LCVR) having an amino acid sequence selected from the group consisting of SEQ ID NO: 10, 26, 42, 58, 74, 90, 106, 122, 138, 154, 170, 186, 202, 218, 234, 250, 266, 282, 298, 314, 330, 346, 362, 378, 394, 410, 426, 442, 458, 474 and 490, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

The present invention also provides an antibody or antigen-binding fragment thereof comprising a HCVR and LCVR (HCVR/LCVR) sequence pair selected from the group consisting of SEQ ID NO: 2/10, 18/26, 34/42, 50/58, 66/74, 82/90, 98/106, 114/122, 130/138, 146/154, 162/170, 178/186, 194/202, 210/218, 226/234, 242/250, 258/266, 274/282, 290/298, 306/314, 322/330, 338/346, 354/362, 370/378, 386/394, 402/410, 418/426, 434/442, 450/458, 466/474 and 482/490.

The present invention also provides an antibody or antigen-binding fragment of an antibody comprising a heavy chain CDR3 (HCDR3) domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 8, 24, 40, 56, 72, 88, 104, 120, 136, 152, 168, 184, 200, 216, 232, 248, 264, 280, 296, 312, 328, 344, 360, 376, 392, 408, 424, 440, 456, 472 and 488 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; and a light chain CDR3 (LCDR3) domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 16, 32, 48, 64, 80, 96, 112, 128, 144, 160, 176, 192, 208, 224, 240, 256, 272, 288, 304, 320, 336, 352, 368, 384, 400, 416, 432, 448, 464, 480 and 496, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

In certain embodiments, the antibody or antigen-binding portion of an antibody comprises a HCDR3/LCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NO: 8/16, 24/32, 40/48, 56/64, 72/80, 88/96, 104/112, 120/128, 136/144, 152/160, 168/176, 184/192, 200/208, 216/224, 232/240, 248/256, 264/272, 280/288, 296/304, 312/320, 328/336, 344/352, 360/368, 376/384, 392/400, 408/416, 424/432, 440/448, 456/464, 472/480 and 488/496.

The present invention also provides an antibody or fragment thereof further comprising a heavy chain CDR1 (HCDR1) domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 4, 20, 36, 52, 68, 84, 100, 116, 132, 148, 164, 180, 196, 212, 228, 244, 260, 276, 292, 308, 324, 340, 356, 372, 388, 404, 420, 436, 452,

468 and 484, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a heavy chain CDR2 (HCDR2) domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 6, 22, 38, 54, 70, 86, 102, 118, 134, 150, 166, 182, 198, 214, 230, 246, 262, 278, 294, 310, 326, 342, 358, 374, 390, 406, 422, 438, 454, 470 and 486, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a light chain CDR1 (LCDR1) domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 12, 28, 44, 60, 76, 92, 108, 124, 140, 156, 172, 188, 204, 220, 236, 252, 268, 284, 300, 316, 332, 348, 364, 380, 396, 412, 428, 444, 460, 476 and 492, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; and a light chain CDR2 (LCDR2) domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 14, 30, 46, 62, 78, 94, 110, 126, 142, 158, 174, 190, 206, 222, 238, 254, 270, 286, 302, 318, 334, 350, 366, 382, 398, 414, 430, 446, 462, 478 and 494, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

Certain non-limiting, exemplary antibodies and antigen-binding fragments of the invention comprise HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 domains, respectively, having the amino acid sequences selected from the group consisting of: SEQ ID NOs: 4-6-8-12-14-16 (e.g. H4H2084P); 20-22-24-28-30-32 (e.g. H4H2092P); 36-38-40-44-46-48 (e.g. H4H2094P); 52-54-56-60-62-64 (e.g. H4H2098P); 68-70-72-76-78-80 (e.g. H4H2102P); 84-86-88-92-94-96 (e.g. H4H2108P); 100-102-104-108-110-112 (e.g. H4H2111P); 116-118-120-124-126-128 (e.g. H4H2114P); 132-134-136-140-142-144 (e.g. H4H2132P); 148-150-152-156-158-160 (e.g., H4H2138P); 164-166-168-172-174-176 (e.g. H4H2140P); 180-182-184-188-190-192 (e.g., H4H2143P); 196-198-200-204-206-208 (e.g. H4H2146P); 212-214-216-220-222-224 (e.g. H4H2147P); 228-230-232-236-238-240 (e.g. H4H2148P); 244-246-248-252-254-256 (e.g. H4H2151P); 260-262-264-268-270-272 (e.g. H4H2153P); 276-278-280-284-286-288 (e.g. H4H2154P); 292-294-296-300-302-304 (e.g. H4H2290P); 308-310-312-316-318-320 (e.g. H1M1819N); 324-326-328-332-334-336 (e.g. H2M1821N); 340-342-344-348-350-352 (e.g. H2M1824N); 356-358-360-364-366-368 (e.g. H2M1827N); 372-374-376-380-382-384 (e.g. H1M1828N); 388-390-392-396-398-400 (e.g. H2M1829N); 404-406-408-412-414-416 (e.g. H2M1930N); 420-422-424-428-430-432 (e.g. H2M1943N); 436-438-440-444-446-448 (e.g. H2M1936N); 452-454-456-460-462-464 (e.g. H2M1937N); 468-470-472-476-478-480 (e.g. H2M1938N); and 484-486-488-492-494-496 (e.g. H1M1940N).

In a related embodiment, the invention includes an antibody or antigen-binding fragment of an antibody which specifically binds ErbB3, wherein the antibody or fragment comprises the heavy and light chain CDR domains contained within heavy and light chain sequences selected from the group consisting of SEQ ID NO: 2/10, 18/26, 34/42, 50/58, 66/74, 82/90, 98/106, 114/122, 130/138, 146/154, 162/170, 178/186, 194/202, 210/218, 226/234, 242/250, 258/266, 274/282, 290/298, 306/314, 322/330, 338/346, 354/362, 370/378, 386/394, 402/410, 418/426, 434/442, 450/458, 466/474 and 482/490. Methods and techniques for identifying CDRs within HCVR and LCVR amino acid sequences are well known in the art and can be used to identify CDRs within the specified HCVR and/or LCVR amino acid sequences disclosed herein. Exemplary conven-

tions that can be used to identify the boundaries of CDRs include, e.g., the Kabat definition, the Chothia definition, and the AbM definition. In general terms, the Kabat definition is based on sequence variability, the Chothia definition is based on the location of the structural loop regions, and the AbM definition is a compromise between the Kabat and Chothia approaches. See, e.g., Kabat, "Sequences of Proteins of Immunological Interest," National Institutes of Health, Bethesda, Md. (1991); Al-Lazikani et al., *J. Mol. Biol.* 273:927-948 (1997); and Martin et al., *Proc. Natl. Acad. Sci. USA* 86:9268-9272 (1989). Public databases are also available for identifying CDR sequences within an antibody.

In another aspect, the invention provides nucleic acid molecules encoding anti-ErbB3 antibodies or fragments thereof. Recombinant expression vectors carrying the nucleic acids of the invention, and host cells into which such vectors have been introduced, are also encompassed by the invention, as are methods of producing the antibodies by culturing the host cells under conditions permitting production of the antibodies, and recovering the antibodies produced.

In one embodiment, the invention provides an antibody or fragment thereof comprising a HCVR encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1, 17, 33, 49, 65, 81, 97, 113, 129, 145, 161, 177, 193, 209, 225, 241, 257, 273, 289, 305, 321, 337, 353, 369, 385, 401, 417, 433, 449, 465 and 481, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof.

The present invention also provides an antibody or fragment thereof comprising a LCVR encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 9, 25, 41, 57, 73, 89, 105, 121, 137, 153, 169, 185, 201, 217, 233, 249, 265, 281, 297, 313, 329, 345, 361, 377, 393, 409, 425, 441, 457, 473 and 489, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof.

The present invention also provides an antibody or antigen-binding fragment of an antibody comprising a HCDR3 domain encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 7, 23, 39, 55, 71, 87, 103, 119, 135, 151, 167, 183, 199, 215, 231, 247, 263, 279, 295, 311, 327, 343, 359, 375, 391, 407, 423, 439, 455, 471 and 478, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof; and a LCDR3 domain encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 15, 31, 47, 63, 79, 95, 111, 127, 143, 159, 175, 191, 207, 223, 239, 255, 271, 287, 303, 319, 335, 351, 367, 383, 399, 415, 431, 447, 463, 479 and 495, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof.

The present invention also provides an antibody or fragment thereof which further comprises a HCDR1 domain encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 3, 19, 35, 51, 67, 83, 99, 115, 131, 147, 163, 179, 195, 211, 227, 243, 259, 275, 291, 307, 323, 339, 355, 371, 387, 403, 419, 435, 451, 467 and 483 or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof; a HCDR2 domain encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 5, 21, 37, 53, 69, 85, 101, 117, 133, 149, 165, 181, 197, 213, 229, 245, 261, 277, 293, 309, 325, 341, 357, 373, 389, 405, 421, 437, 453, 469 and 485, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99%

homology thereof; a LCDR1 domain encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 11, 27, 43, 59, 75, 91, 107, 123, 139, 155, 171, 187, 203, 219, 235, 251, 267, 283, 299, 315, 331, 347, 363, 379, 395, 411, 427, 443, 459, 475 and 491, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof; and a LCDR2 domain encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 13, 29, 45, 61, 77, 93, 109, 125, 141, 157, 173, 189, 205, 221, 237, 253, 269, 285, 301, 317, 333, 349, 365, 381, 397, 413, 429, 445, 461, 477 and 493, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof.

According to certain embodiments, the antibody or fragment thereof comprises the heavy and light chain CDR sequences encoded by the nucleic acid sequences of SEQ ID NOs: SEQ ID NOs: 1 and 9 (e.g. H4H2084P), 17 and 25 (e.g. H4H2092P), 33 and 41 (e.g. H4H2094P), 49 and 57 (e.g. H4H2098P), 65 and 73 (e.g. H4H2102P), 81 and 89 (e.g. H4H2108P), 97 and 105 (e.g. H4H2111P), 113 and 121 (e.g. H4H2114P), 129 and 137 (e.g. H4H2132P), 145 and 153 (e.g. H4H2138P), 161 and 169 (e.g. H4H2140P), 177 and 185 (e.g. H4H2143P), 193 and 201 (e.g. H4H2146P), 209 and 217 (e.g. H4H2147P), 225 and 233 (e.g. H4H2148P), 241 and 249 (e.g. H4H2151P), 257 and 265 (e.g. H4H2153P), 273 and 281 (e.g. H4H2154P), 289 and 297 (e.g. H4H2290P), 305 and 313 (e.g. H1M1819N), 321 and 329 (e.g. H2M1821N), 337 and 345 (e.g. H2M1824N), 353 and 361 (e.g. H2M1827N), 369 and 377 (e.g. H1M1828N), 385 and 393 (e.g. H2M1829N), 401 and 409 (e.g. H2M1930N), 417 and 425 (e.g. H2M1934N), 433 and 441 (e.g. H2M1936N), 449 and 457 (e.g. H2M1937N), 465 and 473 (e.g. H2M1938N), or 481 and 489 (e.g. H1M1940N).

The present invention includes anti-ErbB3 antibodies having a modified glycosylation pattern. In some applications, modification to remove undesirable glycosylation sites may be useful, or an antibody lacking a fucose moiety present on the oligosaccharide chain, for example, to increase antibody dependent cellular cytotoxicity (ADCC) function (see Shield et al. (2002) JBC 277:26733). In other applications, modification of galactosylation can be made in order to modify complement dependent cytotoxicity (CDC).

In another aspect, the invention provides a pharmaceutical composition comprising a recombinant human antibody or fragment thereof which specifically binds ErbB3 and a pharmaceutically acceptable carrier. In a related aspect, the invention features a composition which is a combination of an ErbB3 inhibitor and a second therapeutic agent. In one embodiment, the ErbB3 inhibitor is an antibody or fragment thereof. In one embodiment, the second therapeutic agent is any agent that is advantageously combined with an ErbB3 inhibitor. Exemplary agents that may be advantageously combined with an ErbB3 inhibitor include, without limitation, other agents inhibit ErbB3 activity (including other antibodies or antigen-binding fragments thereof, peptide inhibitors, small molecule antagonists, etc) and/or agents which interfere with ErbB3 upstream or downstream signaling.

In yet another aspect, the invention provides methods for inhibiting ErbB3 activity using an anti-ErbB3 antibody or antigen-binding portion of an antibody of the invention, wherein the therapeutic methods comprise administering a therapeutically effective amount of a pharmaceutical composition comprising an antibody or antigen-binding fragment of an antibody of the invention. The disorder treated is

any disease or condition which is improved, ameliorated, inhibited or prevented by removal, inhibition or reduction of ErbB3 activity. The anti-ErbB3 antibody or antibody fragment of the invention may function to block the interaction between ErbB3 and an ErbB3 binding partner (e.g., neuregulin-1), or otherwise inhibit the signaling activity of ErbB3.

The present invention also includes the use of an anti-ErbB3 antibody or antigen binding portion of an antibody of the invention in the manufacture of a medicament for the treatment of a disease or disorder related to or caused by ErbB3 activity in a patient.

Other embodiments will become apparent from a review of the ensuing detailed description.

DETAILED DESCRIPTION

Before the present invention is described, it is to be understood that this invention is not limited to particular methods and experimental conditions described, as such methods and conditions may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. As used herein, the term "about," when used in reference to a particular recited numerical value, means that the value may vary from the recited value by no more than 1%. For example, as used herein, the expression "about 100" includes 99 and 101 and all values in between (e.g., 99.1, 99.2, 99.3, 99.4, etc.).

Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. All patents, applications and non-patent publications mentioned in this specification are incorporated herein by reference in their entireties.

Definitions

The expressions "ErbB3" and "ErbB3 fragment," as used herein refer to the human ErbB3 protein or fragment unless specified as being from a non-human species (e.g., "mouse ErbB3," "mouse ErbB3 fragment," "monkey ErbB3," "monkey ErbB3 fragment," etc.). The extracellular domain of human ErbB3 has the amino acid sequence shown in, e.g., amino acids 1-613 of SEQ ID NOs:497-499.

The term "ErbB3 ligand," as used herein, means a protein capable of binding to the extracellular domain of human ErbB3 protein to transmit a biological signal in vivo. The term "ErbB3 ligand" includes neuregulin-1 (NRG1) and neuregulin-2 (NRG2).

The term "antibody", as used herein, is intended to refer to immunoglobulin molecules comprising four polypeptide chains, two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds, as well as multimers thereof (e.g., IgM). Each heavy chain comprises a heavy chain variable region (abbreviated herein as HCVR or V_H) and a heavy chain constant region. The heavy chain constant region comprises three domains, C_{H1} , C_{H2} and C_{H3} . Each light chain comprises a light chain variable region (abbreviated herein as LCVR or V_L) and a light chain constant region. The light chain constant region comprises one domain (C_{L1}). The V_H and V_L regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDRs), interspersed with

regions that are more conserved, termed framework regions (FR). Each V_H and V_L is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. In different embodiments of the invention, the FRs of the anti-ErbB3 antibody (or antigen-binding portion thereof) may be identical to the human germline sequences, or may be naturally or artificially modified. An amino acid consensus sequence may be defined based on a side-by-side analysis of two or more CDRs.

The term "antibody," as used herein, also includes antigen-binding fragments of full antibody molecules. The terms "antigen-binding portion" of an antibody, "antigen-binding fragment" of an antibody, and the like, as used herein, include any naturally occurring, enzymatically obtainable, synthetic, or genetically engineered polypeptide or glycoprotein that specifically binds an antigen to form a complex. Antigen-binding fragments of an antibody may be derived, e.g., from full antibody molecules using any suitable standard techniques such as proteolytic digestion or recombinant genetic engineering techniques involving the manipulation and expression of DNA encoding antibody variable and optionally constant domains. Such DNA is known and/or is readily available from, e.g., commercial sources, DNA libraries (including, e.g., phage-antibody libraries), or can be synthesized. The DNA may be sequenced and manipulated chemically or by using molecular biology techniques, for example, to arrange one or more variable and/or constant domains into a suitable configuration, or to introduce codons, create cysteine residues, modify, add or delete amino acids, etc.

Non-limiting examples of antigen-binding fragments include: (i) Fab fragments; (ii) F(ab')₂ fragments; (iii) Fd fragments; (iv) Fv fragments; (v) single-chain Fv (scFv) molecules; (vi) dAb fragments; and (vii) minimal recognition units consisting of the amino acid residues that mimic the hypervariable region of an antibody (e.g., an isolated complementarity determining region (CDR) such as a CDR3 peptide), or a constrained FR3-CDR3-FR4 peptide. Other engineered molecules, such as domain-specific antibodies, single domain antibodies, domain-deleted antibodies, chimeric antibodies, CDR-grafted antibodies, diabodies, triabodies, tetrabodies, minibodies, nanobodies (e.g. monovalent nanobodies, bivalent nanobodies, etc.), small modular immunopharmaceuticals (SMIPs), and shark variable IgNAR domains, are also encompassed within the expression "antigen-binding fragment," as used herein.

An antigen-binding fragment of an antibody will typically comprise at least one variable domain. The variable domain may be of any size or amino acid composition and will generally comprise at least one CDR which is adjacent to or in frame with one or more framework sequences. In antigen-binding fragments having a V_H domain associated with a V_L domain, the V_H and V_L domains may be situated relative to one another in any suitable arrangement. For example, the variable region may be dimeric and contain V_H - V_H , V_H - V_L or V_L - V_L dimers. Alternatively, the antigen-binding fragment of an antibody may contain a monomeric V_H or V_L domain.

In certain embodiments, an antigen-binding fragment of an antibody may contain at least one variable domain covalently linked to at least one constant domain. Non-limiting, exemplary configurations of variable and constant domains that may be found within an antigen-binding fragment of an antibody of the present invention include: (i) V_H - C_H1 ; (ii) V_H - C_H2 ; (iii) V_H - C_H3 ; (iv) V_H - C_H1 - C_H2 ; (v) V_H - C_H1 - C_H2 - C_H3 ; (vi) V_H - C_H2 - C_H3 ; (vii) V_H - C_L ; (viii)

V_L - C_H1 ; (ix) V_L - C_H2 ; (x) V_L - C_H3 ; (xi) V_L - C_H1 - C_H2 ; (xii) V_L - C_H1 - C_H2 - C_H3 ; (xiii) V_L - C_H2 - C_H3 ; and (xiv) V_L - C_L . In any configuration of variable and constant domains, including any of the exemplary configurations listed above, the variable and constant domains may be either directly linked to one another or may be linked by a full or partial hinge or linker region. A hinge region may consist of at least 2 (e.g., 5, 10, 15, 20, 40, 60 or more) amino acids which result in a flexible or semi-flexible linkage between adjacent variable and/or constant domains in a single polypeptide molecule. Moreover, an antigen-binding fragment of an antibody of the present invention may comprise a homo-dimer or heterodimer (or other multimer) of any of the variable and constant domain configurations listed above in non-covalent association with one another and/or with one or more monomeric V_H or V_L domain (e.g., by disulfide bond(s)).

As with full antibody molecules, antigen-binding fragments may be monospecific or multispecific (e.g., bispecific). A multispecific antigen-binding fragment of an antibody will typically comprise at least two different variable domains, wherein each variable domain is capable of specifically binding to a separate antigen or to a different epitope on the same antigen. Any multispecific antibody format, including the exemplary bispecific antibody formats disclosed herein, may be adapted for use in the context of an antigen-binding fragment of an antibody of the present invention using routine techniques available in the art.

The antibodies of the present invention may function through complement-dependent cytotoxicity (CDC) or antibody-dependent cell-mediated cytotoxicity (ADCC). "Complement-dependent cytotoxicity" (CDC) refers to lysis of antigen-expressing cells by an antibody of the invention in the presence of complement. "Antibody-dependent cell-mediated cytotoxicity" (ADCC) refers to a cell-mediated reaction in which nonspecific cytotoxic cells that express Fc receptors (FcRs) (e.g., Natural Killer (NK) cells, neutrophils, and macrophages) recognize bound antibody on a target cell and thereby lead to lysis of the target cell. CDC and ADCC can be measured using assays that are well known and available in the art. (See, e.g., U.S. Pat. Nos. 5,500,362 and 5,821,337, and Clynes et al. (1998) Proc. Natl. Acad. Sci. (USA) 95:652-656). The constant region of an antibody is important in the ability of an antibody to fix complement and mediate cell-dependent cytotoxicity. Thus, the isotype of an antibody may be selected on the basis of whether it is desirable for the antibody to mediate cytotoxicity.

The term "human antibody", as used herein, is intended to include antibodies having variable and constant regions derived from human germline immunoglobulin sequences. The human antibodies of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo), for example in the CDRs and in particular CDR3. However, the term "human antibody", as used herein, is not intended to include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences.

The term "recombinant human antibody", as used herein, is intended to include all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as antibodies expressed using a recombinant expression vector transfected into a host cell (described further below), antibodies isolated from a recombinant, combinatorial human antibody library (described further below), antibod-

ies isolated from an animal (e.g., a mouse) that is transgenic for human immunoglobulin genes (see e.g., Taylor et al. (1992) Nucl. Acids Res. 20:6287-6295) or antibodies prepared, expressed, created or isolated by any other means that involves splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant human antibodies have variable and constant regions derived from human germline immunoglobulin sequences. In certain embodiments, however, such recombinant human antibodies are subjected to in vitro mutagenesis (or, when an animal transgenic for human Ig sequences is used, in vivo somatic mutagenesis) and thus the amino acid sequences of the V_H and V_L regions of the recombinant antibodies are sequences that, while derived from and related to human germline V_H and V_L sequences, may not naturally exist within the human antibody germline repertoire in vivo.

Human antibodies can exist in two forms that are associated with hinge heterogeneity. In one form, an immunoglobulin molecule comprises a stable four chain construct of approximately 150-160 kDa in which the dimers are held together by an interchain heavy chain disulfide bond. In a second form, the dimers are not linked via inter-chain disulfide bonds and a molecule of about 75-80 kDa is formed composed of a covalently coupled light and heavy chain (half-antibody). These forms have been extremely difficult to separate, even after affinity purification.

The frequency of appearance of the second form in various intact IgG isotypes is due to, but not limited to, structural differences associated with the hinge region isotype of the antibody. A single amino acid substitution in the hinge region of the human IgG4 hinge can significantly reduce the appearance of the second form (Angal et al. (1993) Molecular Immunology 30:105) to levels typically observed using a human IgG1 hinge. The instant invention encompasses antibodies having one or more mutations in the hinge, C_H2 or C_H3 region which may be desirable, for example, in production, to improve the yield of the desired antibody form.

An "isolated antibody," as used herein, means an antibody that has been identified and separated and/or recovered from at least one component of its natural environment. For example, an antibody that has been separated or removed from at least one component of an organism, or from a tissue or cell in which the antibody naturally exists or is naturally produced, is an "isolated antibody" for purposes of the present invention. An isolated antibody also includes an antibody in situ within a recombinant cell. Isolated antibodies are antibodies that have been subjected to at least one purification or isolation step. According to certain embodiments, an isolated antibody may be substantially free of other cellular material and/or chemicals.

The term "specifically binds," or the like, means that an antibody or antigen-binding fragment thereof forms a complex with an antigen that is relatively stable under physiologic conditions. Methods for determining whether an antibody specifically binds to an antigen are well known in the art and include, for example, equilibrium dialysis, surface plasmon resonance, and the like. For example, an antibody that "specifically binds" human ErbB3, as used in the context of the present invention, includes antibodies that bind human ErbB3 or portion thereof with a KD of less than about 1000 nM, less than about 500 nM, less than about 300 nM, less than about 200 nM, less than about 100 nM, less than about 90 nM, less than about 80 nM, less than about 70 nM, less than about 60 nM, less than about 50 nM, less than about 40 nM, less than about 30 nM, less than about 20 nM, less than about 10 nM, less than about 5 nM, less than about

4 nM, less than about 3 nM, less than about 2 nM, less than about 1 nM or less than about 0.5 nM, as measured in a surface plasmon resonance assay. (See, e.g., Example 3, herein). An isolated antibody that specifically binds human ErbB3 may, however, have cross-reactivity to other antigens, such as ErbB3 molecules from other (non-human) species.

A "neutralizing" or "blocking" antibody, as used herein, is intended to refer to an antibody whose binding to ErbB3: (i) interferes with the interaction between ErbB3 or an ErbB3 fragment and an ErbB3 ligand (e.g., neuregulin 1), and/or (ii) results in inhibition of at least one biological function of ErbB3. The inhibition caused by an ErbB3 neutralizing or blocking antibody need not be complete so long as it is detectable using an appropriate assay. Exemplary assays for detecting ErbB3 inhibition are described herein.

The anti-ErbB3 antibodies disclosed herein may comprise one or more amino acid substitutions, insertions and/or deletions in the framework and/or CDR regions of the heavy and light chain variable domains as compared to the corresponding germline sequences from which the antibodies were derived. Such mutations can be readily ascertained by comparing the amino acid sequences disclosed herein to germline sequences available from, for example, public antibody sequence databases. The present invention includes antibodies, and antigen-binding fragments thereof, which are derived from any of the amino acid sequences disclosed herein, wherein one or more amino acids within one or more framework and/or CDR regions are mutated to the corresponding residue(s) of the germline sequence from which the antibody was derived, or to the corresponding residue(s) of another human germline sequence, or to a conservative amino acid substitution of the corresponding germline residue(s) (such sequence changes are referred to herein collectively as "germline mutations"). A person of ordinary skill in the art, starting with the heavy and light chain variable region sequences disclosed herein, can easily produce numerous antibodies and antigen-binding fragments which comprise one or more individual germline mutations or combinations thereof. In certain embodiments, all of the framework and/or CDR residues within the V_H and/or V_L domains are mutated back to the residues found in the original germline sequence from which the antibody was derived. In other embodiments, only certain residues are mutated back to the original germline sequence, e.g., only the mutated residues found within the first 8 amino acids of FR1 or within the last 8 amino acids of FR4, or only the mutated residues found within CDR1, CDR2 or CDR3. In other embodiments, one or more of the framework and/or CDR residue(s) are mutated to the corresponding residue(s) of a different germline sequence (i.e., a germline sequence that is different from the germline sequence from which the antibody was originally derived). Furthermore, the antibodies of the present invention may contain any combination of two or more germline mutations within the framework and/or CDR regions, e.g., wherein certain individual residues are mutated to the corresponding residue of a particular germline sequence while certain other residues that differ from the original germline sequence are maintained or are mutated to the corresponding residue of a different germline sequence. Once obtained, antibodies and antigen-binding fragments that contain one or more germline mutations can be easily tested for one or more desired property such as, improved binding specificity, increased binding affinity, improved or enhanced antagonistic or agonistic biological properties (as the case may be), reduced immunogenicity,

etc. Antibodies and antigen-binding fragments obtained in this general manner are encompassed within the present invention.

The present invention also includes anti-ErbB3 antibodies comprising variants of any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein having one or more conservative substitutions. For example, the present invention includes anti-ErbB3 antibodies having HCVR, LCVR, and/or CDR amino acid sequences with, e.g., 10 or fewer, 8 or fewer, 6 or fewer, 4 or fewer, etc. conservative amino acid substitutions relative to any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein.

The term “surface plasmon resonance”, as used herein, refers to an optical phenomenon that allows for the analysis of real-time interactions by detection of alterations in protein concentrations within a biosensor matrix, for example using the BIAcore™ system (Biacore Life Sciences division of GE Healthcare, Piscataway, N.J.).

The term “ K_D ”, as used herein, is intended to refer to the equilibrium dissociation constant of a particular antibody-antigen interaction.

The term “epitope” refers to an antigenic determinant that interacts with a specific antigen binding site in the variable region of an antibody molecule known as a paratope. A single antigen may have more than one epitope. Thus, different antibodies may bind to different areas on an antigen and may have different biological effects. Epitopes may be either conformational or linear. A conformational epitope is produced by spatially juxtaposed amino acids from different segments of the linear polypeptide chain. A linear epitope is one produced by adjacent amino acid residues in a polypeptide chain. In certain circumstance, an epitope may include moieties of saccharides, phosphoryl groups, or sulfonyl groups on the antigen.

The term “substantial identity” or “substantially identical,” when referring to a nucleic acid or fragment thereof, indicates that, when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 95%, and more preferably at least about 96%, 97%, 98% or 99% of the nucleotide bases, as measured by any well-known algorithm of sequence identity, such as FASTA, BLAST or Gap, as discussed below. A nucleic acid molecule having substantial identity to a reference nucleic acid molecule may, in certain instances, encode a polypeptide having the same or substantially similar amino acid sequence as the polypeptide encoded by the reference nucleic acid molecule.

As applied to polypeptides, the term “substantial similarity” or “substantially similar” means that two peptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 95% sequence identity, even more preferably at least 98% or 99% sequence identity. Preferably, residue positions which are not identical differ by conservative amino acid substitutions. A “conservative amino acid substitution” is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of similarity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well-known to those of skill in the art. See, e.g., Pearson (1994) Methods

Mol. Biol. 24: 307-331, herein incorporated by reference. Examples of groups of amino acids that have side chains with similar chemical properties include (1) aliphatic side chains: glycine, alanine, valine, leucine and isoleucine; (2) aliphatic-hydroxyl side chains: serine and threonine; (3) amide-containing side chains: asparagine and glutamine; (4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; (5) basic side chains: lysine, arginine, and histidine; (6) acidic side chains: aspartate and glutamate, and (7) sulfur-containing side chains are cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine. Alternatively, a conservative replacement is any change having a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet et al. (1992) Science 256: 1443-1445, herein incorporated by reference. A “moderately conservative” replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

Sequence similarity for polypeptides, which is also referred to as sequence identity, is typically measured using sequence analysis software. Protein analysis software matches similar sequences using measures of similarity assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG software contains programs such as Gap and Bestfit which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutein thereof. See, e.g., GCG Version 6.1. Polypeptide sequences also can be compared using FASTA using default or recommended parameters, a program in GCG Version 6.1. FASTA (e.g., FASTA2 and FASTA3) provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson (2000) supra). Another preferred algorithm when comparing a sequence of the invention to a database containing a large number of sequences from different organisms is the computer program BLAST, especially BLASTP or TBLASTN, using default parameters. See, e.g., Altschul et al. (1990) J. Mol. Biol. 215:403-410 and Altschul et al. (1997) Nucleic Acids Res. 25:3389-402, each herein incorporated by reference.

Biological Characteristics of the Antibodies

The antibodies of the present invention block the interaction between ErbB3 and its ligand neuregulin-1 (NRG1). As used herein, the expression “blocks the interaction between ErbB3 and NRG1” means that, in an assay in which the physical interaction between ErbB3 and NRG1 can be detected and/or quantified, the addition of an antibody of the invention reduces the interaction between ErbB3 and NRG1 by at least 50%. A non-limiting, exemplary assay that can be used to determine if an antibody blocks the interaction between human ErbB3 and NRG1 is illustrated in Example 4, herein. In this Example, antibodies are mixed with ErbB3 protein, and then the antibody/ErbB3 mixture is applied to a surface coated with NRG1 protein. After washing away unbound molecules, the amount of ErbB3 bound to the NRG1-coated surface is measured. By using varying amounts of antibody in this assay format, the amount of antibody required to block 50% of ErbB3 binding to NRG1 can be calculated and expressed as an IC_{50} value. The present invention includes anti-ErbB3 antibodies that exhibit an IC_{50} of less than about 600 pM when tested in an ErbB3/NRG1 binding assay as described above, or a substantially similar assay. For example, the invention includes

anti-ErbB3 antibodies that exhibit an IC_{50} of less than about 600, 500, 400, 300, 290, 280, 270, 260, 250, 240, 230, 220, 210, 200, 190, 180, 170, 160, 150, 140, 130, 120, 110, 100, 90, 80, 70, 60, 50, 40, 30, 20, 10, 18, 16, 14, 12, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 pM when tested in an ErbB3/NRG1 binding assay as described above, or a substantially similar assay.

Alternatively, one can determine whether an antibody blocks the interaction between ErbB3 and NRG1 by using a cell-based assay format that detects changes in NRG1-induced cellular signaling. Exemplary assay formats of this type are illustrated in Examples 6 and 8, herein. In these Examples, the extent of phosphorylation of the kinase Akt and/or ErbB3 in cells following treatment with NRG1 in the presence of varying amounts of anti-ErbB3 antibody is measured. In these assay formats, the percent inhibition of Akt and/or ErbB3 phosphorylation caused by the presence of an anti-ErbB3 antibody serves as an indicator of the extent to which the antibody blocks the interaction between ErbB3 and NRG1. The present invention includes antibodies that inhibit Akt or ErbB3 phosphorylation by at least 60% when tested in an Akt or ErbB3 phosphorylation assay as described above, or a substantially similar assay. For example, the invention includes anti-ErbB3 antibodies that inhibit Akt or ErbB3 phosphorylation by at least about 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% when tested in an Akt or ErbB3 phosphorylation assay as described above, or a substantially similar assay.

The anti-ErbB3 antibodies of the present invention also exhibit one or more of the following properties: (1) the ability to induce internalization of cell surface expressed ErbB3 (see, e.g., Example 5, herein); (2) the ability to inhibit NRG1-stimulated tumor cell growth in vitro, either alone or in combination with EGFR inhibition (see, e.g., Example 7, herein); and (3) the ability to inhibit tumor growth in animals (see, e.g., Example 9, herein).

Epitope Mapping and Related Technologies

The ErbB3 protein, like all ErbB/HER family members, contains four extracellular domains, referred to as "Domain I," "Domain II," "Domain III," and "Domain IV." Domain I is the sequence of amino acids represented by amino acids 1 through 190 of SEQ ID NO:498; Domain II is the sequence of amino acids represented by amino acids 191 through 308 of SEQ ID NO:498; Domain III is the sequence of amino acids represented by amino acids 309 through 499 of SEQ ID NO:498; and Domain IV is the sequence of amino acids represented by amino acids 500 through 624 of SEQ ID NO:498.

The present invention includes anti-ErbB3 antibodies which interact with one or more epitopes found within Domain III of the extracellular domain of ErbB3. The epitope(s) may consist of one or more contiguous sequences of 3 or more (e.g., 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more) amino acids located within Domain III of ErbB3. Alternatively, the epitope may consist of a plurality of non-contiguous amino acids (or amino acid sequences) located within Domain III of ErbB3. According to certain embodiments of the present invention, anti-ErbB3 antibodies are provided which interact with one or more amino acids located within one or more Domain III amino acid segments selected from the group consisting of amino acids 345-367 of SEQ ID NO:498, amino acids 423-439 of SEQ ID NO:498; and amino acids 451-463 of SEQ ID NO:498. For example, the present invention includes anti-ErbB3 antibodies which interact with at least one amino acid within each of the aforementioned Domain III amino acid segments (i.e., within each of amino acids 345-367, 423-439, and 451-463 of SEQ ID NO:498).

Various techniques known to persons of ordinary skill in the art can be used to determine whether an antibody "interacts with one or more amino acids" within a polypeptide or protein. Exemplary techniques include, e.g., routine cross-blocking assay such as that described *Antibodies*, Harlow and Lane (Cold Spring Harbor Press, Cold Spring Harbor, NY), alanine scanning mutational analysis, peptide blots analysis (Reineke, 2004, *Methods Mol Biol* 248:443-463), and peptide cleavage analysis. In addition, methods such as epitope excision, epitope extraction and chemical modification of antigens can be employed (Tomer, 2000, *Protein Science* 9:487-496). Another method that can be used to identify the amino acids within a polypeptide with which an antibody interacts is hydrogen/deuterium exchange detected by mass spectrometry. (See, e.g., Example 11 herein). In general terms, the hydrogen/deuterium exchange method involves deuterium-labeling the protein of interest, followed by binding the antibody to the deuterium-labeled protein. Next, the protein/antibody complex is transferred to water to allow hydrogen-deuterium exchange to occur at all residues except for the residues protected by the antibody (which remain deuterium-labeled). After dissociation of the antibody, the target protein is subjected to protease cleavage and mass spectrometry analysis, thereby revealing the deuterium-labeled residues which correspond to the specific amino acids with which the antibody interacts. See, e.g., Ehring (1999) *Analytical Biochemistry* 267(2):252-259; Engen and Smith (2001) *Anal. Chem.* 73:256A-265A.

The present invention further includes anti-ErbB3 antibodies that bind to the same epitope as any of the specific exemplary antibodies described herein (e.g., H1M1819N, H2M1821N, H2M1824N, H2M1827N, H1M1828N, H2M1829N, H2M1930N, H2M1934N, H2M1938N, H1M1940N, etc.). Likewise, the present invention also includes anti-ErbB3 antibodies that compete for binding to ErbB3 or an ErbB3 fragment with any of the specific exemplary antibodies described herein (e.g., H1M1819N, H2M1821N, H2M1824N, H2M1827N, H1M1828N, H2M1829N, H2M1930N, H2M1934N, H2M1938N, H1M1940N, etc.).

One can easily determine whether an antibody binds to the same epitope as, or competes for binding with, a reference anti-ErbB3 antibody by using routine methods known in the art. For example, to determine if a test antibody binds to the same epitope as a reference anti-ErbB3 antibody of the invention, the reference antibody is allowed to bind to an ErbB3 protein or peptide under saturating conditions. Next, the ability of a test antibody to bind to the ErbB3 molecule is assessed. If the test antibody is able to bind to ErbB3 following saturation binding with the reference anti-ErbB3 antibody, it can be concluded that the test antibody binds to a different epitope than the reference anti-ErbB3 antibody. On the other hand, if the test antibody is not able to bind to the ErbB3 molecule following saturation binding with the reference anti-ErbB3 antibody, then the test antibody may bind to the same epitope as the epitope bound by the reference anti-ErbB3 antibody of the invention. Additional routine experimentation (e.g., peptide mutation and binding analyses) can then be carried out to confirm whether the observed lack of binding of the test antibody is in fact due to binding to the same epitope as the reference antibody or if steric blocking (or another phenomenon) is responsible for the lack of observed binding. Experiments of this sort can be performed using ELISA, RIA, Biacore, flow cytometry or any other quantitative or qualitative antibody-binding assay available in the art. In accordance with certain embodiments

of the present invention, two antibodies bind to the same (or overlapping) epitope if, e.g., a 1-, 5-, 10-, 20- or 100-fold excess of one antibody inhibits binding of the other by at least 50% but preferably 75%, 90% or even 99% as measured in a competitive binding assay (see, e.g., Junghans et al., *Cancer Res.* 1990:50:1495-1502). Alternatively, two antibodies are deemed to bind to the same epitope if essentially all amino acid mutations in the antigen that reduce or eliminate binding of one antibody reduce or eliminate binding of the other. Two antibodies are deemed to have “overlapping epitopes” if only a subset of the amino acid mutations that reduce or eliminate binding of one antibody reduce or eliminate binding of the other.

To determine if an antibody competes for binding with a reference anti-ErbB3 antibody, the above-described binding methodology is performed in two orientations: In a first orientation, the reference antibody is allowed to bind to an ErbB3 molecule under saturating conditions followed by assessment of binding of the test antibody to the ErbB3 molecule. In a second orientation, the test antibody is allowed to bind to an ErbB3 molecule under saturating conditions followed by assessment of binding of the reference antibody to the ErbB3 molecule. If, in both orientations, only the first (saturating) antibody is capable of binding to the ErbB3 molecule, then it is concluded that the test antibody and the reference antibody compete for binding to ErbB3. As will be appreciated by a person of ordinary skill in the art, an antibody that competes for binding with a reference antibody may not necessarily bind to the same epitope as the reference antibody, but may sterically block binding of the reference antibody by binding an overlapping or adjacent epitope.

Preparation of Human Antibodies

Methods for generating monoclonal antibodies, including fully human monoclonal antibodies are known in the art. Any such known methods can be used in the context of the present invention to make human antibodies that specifically bind to human ErbB3.

Using VELOCIMMUNE™ technology or any other known method for generating monoclonal antibodies, high affinity chimeric antibodies to ErbB3 are initially isolated having a human variable region and a mouse constant region. As in the experimental section below, the antibodies are characterized and selected for desirable characteristics, including affinity, selectivity, epitope, etc. The mouse constant regions are replaced with a desired human constant region to generate the fully human antibody of the invention, for example wild-type or modified IgG1 or IgG4. While the constant region selected may vary according to specific use, high affinity antigen-binding and target specificity characteristics reside in the variable region.

Bioequivalents

The anti-ErbB3 antibodies and antibody fragments of the present invention encompass proteins having amino acid sequences that vary from those of the described antibodies but that retain the ability to bind human ErbB3. Such variant antibodies and antibody fragments comprise one or more additions, deletions, or substitutions of amino acids when compared to parent sequence, but exhibit biological activity that is essentially equivalent to that of the described antibodies. Likewise, the anti-ErbB3 antibody-encoding DNA sequences of the present invention encompass sequences that comprise one or more additions, deletions, or substitutions of nucleotides when compared to the disclosed sequence, but that encode an anti-ErbB3 antibody or antibody fragment that is essentially bioequivalent to an anti-

ErbB3 antibody or antibody fragment of the invention. Examples of such variant amino acid and DNA sequences are discussed above.

Two antigen-binding proteins, or antibodies, are considered bioequivalent if, for example, they are pharmaceutical equivalents or pharmaceutical alternatives whose rate and extent of absorption do not show a significant difference when administered at the same molar dose under similar experimental conditions, either single dose or multiple dose. Some antibodies will be considered equivalents or pharmaceutical alternatives if they are equivalent in the extent of their absorption but not in their rate of absorption and yet may be considered bioequivalent because such differences in the rate of absorption are intentional and are reflected in the labeling, are not essential to the attainment of effective body drug concentrations on, e.g., chronic use, and are considered medically insignificant for the particular drug product studied.

In one embodiment, two antigen-binding proteins are bioequivalent if there are no clinically meaningful differences in their safety, purity, and potency.

In one embodiment, two antigen-binding proteins are bioequivalent if a patient can be switched one or more times between the reference product and the biological product without an expected increase in the risk of adverse effects, including a clinically significant change in immunogenicity, or diminished effectiveness, as compared to continued therapy without such switching.

In one embodiment, two antigen-binding proteins are bioequivalent if they both act by a common mechanism or mechanisms of action for the condition or conditions of use, to the extent that such mechanisms are known.

Bioequivalence may be demonstrated by *in vivo* and *in vitro* methods. Bioequivalence measures include, e.g., (a) an *in vivo* test in humans or other mammals, in which the concentration of the antibody or its metabolites is measured in blood, plasma, serum, or other biological fluid as a function of time; (b) an *in vitro* test that has been correlated with and is reasonably predictive of human *in vivo* bioavailability data; (c) an *in vivo* test in humans or other mammals in which the appropriate acute pharmacological effect of the antibody (or its target) is measured as a function of time; and (d) in a well-controlled clinical trial that establishes safety, efficacy, or bioavailability or bioequivalence of an antibody.

Bioequivalent variants of anti-ErbB3 antibodies of the invention may be constructed by, for example, making various substitutions of residues or sequences or deleting terminal or internal residues or sequences not needed for biological activity. For example, cysteine residues not essential for biological activity can be deleted or replaced with other amino acids to prevent formation of unnecessary or incorrect intramolecular disulfide bridges upon renaturation. In other contexts, bioequivalent antibodies may include anti-ErbB3 antibody variants comprising amino acid changes which modify the glycosylation characteristics of the antibodies, e.g., mutations which eliminate or remove glycosylation.

Species Selectivity and Species Cross-Reactivity

According to certain embodiments of the invention, the anti-ErbB3 antibodies bind to human ErbB3 but not to ErbB3 from other species. The present invention also includes anti-ErbB3 antibodies that bind to human ErbB3 and to ErbB3 from one or more non-human species. For example, the anti-ErbB3 antibodies of the invention may bind to human ErbB3 and may bind or not bind, as the case may be, to one or more of mouse, rat, guinea pig, hamster,

gerbil, pig, cat, dog, rabbit, goat, sheep, cow, horse, camel, cynomologous, marmoset, rhesus or chimpanzee ErbB3.

Immunoconjugates

The invention encompasses anti-ErbB3 monoclonal antibodies conjugated to a therapeutic moiety (“immunoconjugate”), such as a cytotoxin, a chemotherapeutic drug, an immunosuppressant or a radioisotope. Cytotoxic agents include any agent that is detrimental to cells. Examples of suitable cytotoxic agents and chemotherapeutic agents for forming immunoconjugates are known in the art, (see for example, WO 05/103081).

Multispecific Antibodies

The antibodies of the present invention may be monospecific, bi-specific, or multispecific. Multispecific antibodies may be specific for different epitopes of one target polypeptide or may contain antigen-binding domains specific for more than one target polypeptide. See, e.g., Tutt et al., 1991, *J. Immunol.* 147:60-69; Kufer et al., 2004, *Trends Biotechnol.* 22:238-244. The anti-ErbB3 antibodies of the present invention can be linked to or co-expressed with another functional molecule, e.g., another peptide or protein. For example, an antibody or fragment thereof can be functionally linked (e.g., by chemical coupling, genetic fusion, noncovalent association or otherwise) to one or more other molecular entities, such as another antibody or antibody fragment to produce a bi-specific or a multispecific antibody with a second binding specificity. For example, the present invention includes bi-specific antibodies wherein one arm of an immunoglobulin is specific for human ErbB3 or a fragment thereof, and the other arm of the immunoglobulin is specific for a second therapeutic target (e.g., EGFR, EGFRvIII, ErbB2/HER2, ErbB4, VEGF or Ang2) or is conjugated to a therapeutic moiety.

An exemplary bi-specific antibody format that can be used in the context of the present invention involves the use of a first immunoglobulin (Ig) C_H3 domain and a second Ig C_H3 domain, wherein the first and second Ig C_H3 domains differ from one another by at least one amino acid, and wherein at least one amino acid difference reduces binding of the bispecific antibody to Protein A as compared to a bi-specific antibody lacking the amino acid difference. In one embodiment, the first Ig C_H3 domain binds Protein A and the second Ig C_H3 domain contains a mutation that reduces or abolishes Protein A binding such as an H95R modification (by IMGT exon numbering; H435R by EU numbering). The second C_H3 may further comprise a Y96F modification (by IMGT; Y436F by EU). Further modifications that may be found within the second C_H3 include: D16E, L18M, N44S, K52N, V57M, and V82I (by IMGT; D356E, L358M, N384S, K392N, V397M, and V422I by EU) in the case of IgG1 antibodies; N44S, K52N, and V82I (IMGT; N384S, K392N, and V422I by EU) in the case of IgG2 antibodies; and Q15R, N44S, K52N, V57M, R69K, E79Q, and V82I (by IMGT; Q355R, N384S, K392N, V397M, R409K, E419Q, and V422I by EU) in the case of IgG4 antibodies. Variations on the bi-specific antibody format described above are contemplated within the scope of the present invention.

Therapeutic Formulation and Administration

The invention provides pharmaceutical compositions comprising the anti-ErbB3 antibodies or antigen-binding fragments thereof of the present invention. The pharmaceutical compositions of the invention are formulated with suitable carriers, excipients, and other agents that provide improved transfer, delivery, tolerance, and the like. A multitude of appropriate formulations can be found in the formulary known to all pharmaceutical chemists: Reming-

ton's Pharmaceutical Sciences, Mack Publishing Company, Easton, Pa. These formulations include, for example, powders, pastes, ointments, jellies, waxes, oils, lipids, lipid (cationic or anionic) containing vesicles (such as LIPOFECTIN™), DNA conjugates, anhydrous absorption pastes, oil-in-water and water-in-oil emulsions, emulsions carbowax (polyethylene glycols of various molecular weights), semi-solid gels, and semi-solid mixtures containing carbowax. See also Powell et al. “Compendium of excipients for parenteral formulations” PDA (1998) *J Pharm Sci Technol* 52:238-311.

The dose of antibody administered to a patient may vary depending upon the age and the size of the patient, target disease, conditions, route of administration, and the like. The preferred dose is typically calculated according to body weight or body surface area. When an antibody of the present invention is used for treating a condition or disease associated with ErbB3 activity in an adult patient, it may be advantageous to intravenously administer the antibody of the present invention normally at a single dose of about 0.01 to about 20 mg/kg body weight, more preferably about 0.02 to about 7, about 0.03 to about 5, or about 0.05 to about 3 mg/kg body weight. Depending on the severity of the condition, the frequency and the duration of the treatment can be adjusted. Effective dosages and schedules for administering anti-ErbB3 antibodies may be determined empirically; for example, patient progress can be monitored by periodic assessment, and the dose adjusted accordingly. Moreover, interspecies scaling of dosages can be performed using well-known methods in the art (e.g., Mordenti et al., 1991, *Pharmaceut. Res.* 8:1351).

Various delivery systems are known and can be used to administer the pharmaceutical composition of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the mutant viruses, receptor mediated endocytosis (see, e.g., Wu et al., 1987, *J. Biol. Chem.* 262:4429-4432). Methods of introduction include, but are not limited to, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The composition may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local.

A pharmaceutical composition of the present invention can be delivered subcutaneously or intravenously with a standard needle and syringe. In addition, with respect to subcutaneous delivery, a pen delivery device readily has applications in delivering a pharmaceutical composition of the present invention. Such a pen delivery device can be reusable or disposable. A reusable pen delivery device generally utilizes a replaceable cartridge that contains a pharmaceutical composition. Once all of the pharmaceutical composition within the cartridge has been administered and the cartridge is empty, the empty cartridge can readily be discarded and replaced with a new cartridge that contains the pharmaceutical composition. The pen delivery device can then be reused. In a disposable pen delivery device, there is no replaceable cartridge. Rather, the disposable pen delivery device comes prefilled with the pharmaceutical composition held in a reservoir within the device. Once the reservoir is emptied of the pharmaceutical composition, the entire device is discarded.

Numerous reusable pen and autoinjector delivery devices have applications in the subcutaneous delivery of a phar-

maceutical composition of the present invention. Examples include, but are not limited to AUTOPEN™ (Owen Mumford, Inc., Woodstock, UK), DISETRONIC™ pen (Disetronic Medical Systems, Bergdorf, Switzerland), HUMALOG MIX 75/25™ pen, HUMALOG™ pen, HUMALIN 70/30™ pen (Eli Lilly and Co., Indianapolis, Ind.), NOVOPEN™ I, II and III (Novo Nordisk, Copenhagen, Denmark), NOVOPEN JUNIOR™ (Novo Nordisk, Copenhagen, Denmark), BD™ pen (Becton Dickinson, Franklin Lakes, N.J.), OPTIPEN™, OPTIPEN PRO™, OPTIPEN STARLET™, and OPTICLIK™ (sanofi-aventis, Frankfurt, Germany), to name only a few. Examples of disposable pen delivery devices having applications in subcutaneous delivery of a pharmaceutical composition of the present invention include, but are not limited to the SOLOSTAR™ pen (sanofi-aventis), the FLEXPEN™ (Novo Nordisk), and the KW IKPEN™ (Eli Lilly), the SURECLICK™ Autoinjector (Amgen, Thousand Oaks, Calif.), the PENLET™ (Haselmeier, Stuttgart, Germany), the EPIPEN (Dey, L. P.), and the HUMIRA™ Pen (Abbott Labs, Abbott Park Ill.), to name only a few.

In certain situations, the pharmaceutical composition can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, supra; Sefton, 1987, CRC Crit. Ref. Biomed. Eng. 14:201). In another embodiment, polymeric materials can be used; see, Medical Applications of Controlled Release, Langer and Wise (eds.), 1974, CRC Pres., Boca Raton, Florida. In yet another embodiment, a controlled release system can be placed in proximity of the composition's target, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, 1984, in Medical Applications of Controlled Release, supra, vol. 2, pp. 115-138). Other controlled release systems are discussed in the review by Langer, 1990, Science 249:1527-1533.

The injectable preparations may include dosage forms for intravenous, subcutaneous, intracutaneous and intramuscular injections, drip infusions, etc. These injectable preparations may be prepared by methods publicly known. For example, the injectable preparations may be prepared, e.g., by dissolving, suspending or emulsifying the antibody or its salt described above in a sterile aqueous medium or an oily medium conventionally used for injections. As the aqueous medium for injections, there are, for example, physiological saline, an isotonic solution containing glucose and other auxiliary agents, etc., which may be used in combination with an appropriate solubilizing agent such as an alcohol (e.g., ethanol), a polyalcohol (e.g., propylene glycol, polyethylene glycol), a nonionic surfactant [e.g., polysorbate 80, HCO-50 (polyoxyethylene (50 mol) adduct of hydrogenated castor oil)], etc. As the oily medium, there are employed, e.g., sesame oil, soybean oil, etc., which may be used in combination with a solubilizing agent such as benzyl benzoate, benzyl alcohol, etc. The injection thus prepared is preferably filled in an appropriate ampoule.

Advantageously, the pharmaceutical compositions for oral or parenteral use described above are prepared into dosage forms in a unit dose suited to fit a dose of the active ingredients. Such dosage forms in a unit dose include, for example, tablets, pills, capsules, injections (ampoules), suppositories, etc. The amount of the aforesaid antibody contained is generally about 5 to about 500 mg per dosage form in a unit dose; especially in the form of injection, it is preferred that the aforesaid antibody is contained in about 5 to about 100 mg and in about 10 to about 250 mg for the other dosage forms.

Therapeutic Uses of the Antibodies

The antibodies of the invention are useful, inter alia, for the treatment, prevention and/or amelioration of any disease or disorder associated with or mediated by ErbB3 activity or treatable by blocking the interaction between ErbB3 and an ErbB3 ligand (e.g., NRG1). The antibodies and antigen-binding fragments of the present invention may be used to treat, e.g., primary and/or metastatic tumors arising in the brain and meninges, oropharynx, lung and bronchial tree, gastrointestinal tract, male and female reproductive tract, muscle, bone, skin and appendages, connective tissue, spleen, immune system, blood forming cells and bone marrow, liver and urinary tract, and special sensory organs such as the eye. In certain embodiments, the antibodies and antigen-binding fragments of the invention are used to treat one or more of the following cancers: renal cell carcinoma, pancreatic carcinoma, breast cancer, head and neck cancer, prostate cancer, malignant gliomas, osteosarcoma, colorectal cancer, gastric cancer (e.g., gastric cancer with MET amplification), malignant mesothelioma, multiple myeloma, ovarian cancer, small cell lung cancer, non-small cell lung cancer (e.g., EGFR-dependent non-small cell lung cancer), synovial sarcoma, thyroid cancer, or melanoma.

The present invention also provides methods for treating a tumor which is resistant to, or has become resistant to anti-EGFR or anti-HER2 therapy. For example, the present invention includes methods which comprise (a) identifying a patient having a tumor which is resistant, or has become resistant, to one or more of an anti-EGFR antibody (e.g., cetuximab), a small molecule inhibitor of EGFR (e.g., erlotinib), an anti-HER2 antibody (e.g. trastuzumab), and/or a small molecule inhibitor of HER2; and (b) administering to the patient an anti-ErbB3 antibody of the present invention, either alone, or in combination with an anti-EGFR antibody (e.g., cetuximab), a small molecule inhibitor of EGFR (e.g., erlotinib), an anti-HER2 antibody (e.g. trastuzumab), and/or a small molecule inhibitor of HER2. Combination therapies are discussed in more detail below.

Combination Therapies

The present invention includes therapeutic administration regimens which comprise administering an anti-ErbB3 antibody of the present invention in combination with at least one additional therapeutically active component. Non-limiting examples of such additional therapeutically active components include other ErbB3 antagonists (e.g., a second anti-ErbB3 antibody or small molecule inhibitor of ErbB3), an antagonist of ErbB2/HER2 (e.g., anti-HER2 antibody [e.g., trastuzumab] or small molecule inhibitor of HER2 activity), an antagonist of ErbB4 (e.g., anti-ErbB4 antibody or small molecule inhibitor of ErbB4 activity), an antagonist of epidermal growth factor receptor (EGFR) (e.g., anti-EGFR antibody [e.g., cetuximab or panitumumab] or small molecule inhibitor of EGFR activity [e.g., erlotinib or gefitinib]), an antagonist of EGFRvIII (e.g., an antibody that specifically binds EGFRvIII), a VEGF antagonist (e.g., a VEGF-Trap, see, e.g., U.S. Pat. No. 7,087,411 (also referred to herein as a "VEGF-inhibiting fusion protein"), anti-VEGF antibody (e.g., bevacizumab), a small molecule kinase inhibitor of VEGF receptor (e.g., sunitinib, sorafenib or pazopanib), or an anti-DLL4 antibody (e.g., an anti-DLL4 antibody disclosed in US 2009/0142354 such as REGN421), etc.). Other agents that may be beneficially administered in combination with the anti-ErbB3 antibodies of the invention include cytokine inhibitors, including small-molecule cytokine inhibitors and antibodies that bind to cytokines such as IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-8, IL-9, IL-11, IL-12, IL-13, IL-17, IL-18, or to their respective receptors. The present invention also includes therapeutic combina-

tions comprising any of the anti-ErbB3 antibodies mentioned herein and an inhibitor of one or more of VEGF, DLL4, EGFR, or any of the aforementioned cytokines, wherein the inhibitor is an aptamer, an antisense molecule, a ribozyme, an siRNA, a peptibody, a nanobody or an antibody fragment (e.g., Fab fragment; F(ab')₂ fragment; Fd fragment; Fv fragment; scFv; dAb fragment; or other engineered molecules, such as diabodies, triabodies, tetrabodies, minibodies and minimal recognition units). The anti-ErbB3 antibodies of the invention may also be administered in combination with antivirals, antibiotics, analgesics, corticosteroids and/or NSAIDs. The anti-ErbB3 antibodies of the invention may also be administered as part of a treatment regimen that also includes radiation treatment and/or conventional chemotherapy. The additional therapeutically active component(s) may be administered prior to, concurrent with, or after the administration of an anti-ErbB3 antibody of the present invention; (for purposes of the present disclosure, such administration regimens are considered the administration of an anti-ErbB3 antibody “in combination with” a therapeutically active component of the invention).

Administration Regimens

According to certain embodiments of the present invention, multiple doses of an anti-ErbB3 antibody may be administered to a subject over a defined time course. The methods according to this aspect of the invention comprise sequentially administering to a subject multiple doses of an anti-ErbB3 antibody. As used herein, “sequentially administering” means that each dose of anti-ErbB3 antibody is administered to the subject at a different point in time, e.g., on different days separated by a predetermined interval (e.g., hours, days, weeks or months). The present invention includes methods which comprise sequentially administering to the patient a single initial dose of an anti-ErbB3 antibody, followed by one or more secondary doses of the anti-ErbB3 antibody, and optionally followed by one or more tertiary doses of the anti-ErbB3 antibody.

The terms “initial dose,” “secondary doses,” and “tertiary doses,” refer to the temporal sequence of administration of the anti-ErbB3 antibody. Thus, the “initial dose” is the dose which is administered at the beginning of the treatment regimen (also referred to as the “baseline dose”); the “secondary doses” are the doses which are administered after the initial dose; and the “tertiary doses” are the doses which are administered after the secondary doses. The initial, secondary, and tertiary doses may all contain the same amount of anti-ErbB3 antibody, but generally may differ from one another in terms of frequency of administration. In certain embodiments, however, the amount of anti-ErbB3 antibody contained in the initial, secondary and/or tertiary doses varies from one another (e.g., adjusted up or down as appropriate) during the course of treatment. In certain embodiments, two or more (e.g., 2, 3, 4, or 5) doses are administered at the beginning of the treatment regimen as “loading doses” followed by subsequent doses that are administered on a less frequent basis (e.g., “maintenance doses”).

In one exemplary embodiment of the present invention, each secondary and/or tertiary dose is administered 1 to 26 (e.g., 1, 1½, 2, 2½, 3, 3½, 4, 4½, 5, 5½, 6, 6½, 7, 7½, 8, 8½, 9, 9½, 10, 10½, 11, 11½, 12, 12½, 13, 13½, 14, 14½, 15, 15½, 16, 16½, 17, 17½, 18, 18½, 19, 19½, 20, 20½, 21, 21½, 22, 22½, 23, 23½, 24, 24½, 25, 25½, 26, 26½, or more) weeks after the immediately preceding dose. The phrase “the immediately preceding dose,” as used herein, means, in a sequence of multiple administrations, the dose of

anti-ErbB3 antibody which is administered to a patient prior to the administration of the very next dose in the sequence with no intervening doses.

The methods according to this aspect of the invention may comprise administering to a patient any number of secondary and/or tertiary doses of an anti-ErbB3 antibody. For example, in certain embodiments, only a single secondary dose is administered to the patient. In other embodiments, two or more (e.g., 2, 3, 4, 5, 6, 7, 8, or more) secondary doses are administered to the patient. Likewise, in certain embodiments, only a single tertiary dose is administered to the patient. In other embodiments, two or more (e.g., 2, 3, 4, 5, 6, 7, 8, or more) tertiary doses are administered to the patient.

In embodiments involving multiple secondary doses, each secondary dose may be administered at the same frequency as the other secondary doses. For example, each secondary dose may be administered to the patient 1 to 2 weeks after the immediately preceding dose. Similarly, in embodiments involving multiple tertiary doses, each tertiary dose may be administered at the same frequency as the other tertiary doses. For example, each tertiary dose may be administered to the patient 2 to 4 weeks after the immediately preceding dose. Alternatively, the frequency at which the secondary and/or tertiary doses are administered to a patient can vary over the course of the treatment regimen. The frequency of administration may also be adjusted during the course of treatment by a physician depending on the needs of the individual patient following clinical examination.

Any of the exemplary anti-ErbB3 antibodies disclosed herein may be used in the context of the foregoing administration regimens.

Diagnostic Uses of the Antibodies

The anti-ErbB3 antibodies of the present invention may also be used to detect and/or measure ErbB3 in a sample, e.g., for diagnostic purposes. For example, an anti-ErbB3 antibody, or fragment thereof, may be used to diagnose a condition or disease characterized by aberrant expression (e.g., over-expression, under-expression, lack of expression, etc.) of ErbB3. Exemplary diagnostic assays for ErbB3 may comprise, e.g., contacting a sample, obtained from a patient, with an anti-ErbB3 antibody of the invention, wherein the anti-ErbB3 antibody is labeled with a detectable label or reporter molecule. Alternatively, an unlabeled anti-ErbB3 antibody can be used in diagnostic applications in combination with a secondary antibody which is itself detectably labeled. The detectable label or reporter molecule can be a radioisotope, such as ³H, ¹⁴C, ³²P, ³⁵S, or ¹²⁵I; a fluorescent or chemiluminescent moiety such as fluorescein isothiocyanate, or rhodamine; or an enzyme such as alkaline phosphatase, beta-galactosidase, horseradish peroxidase, or luciferase. Specific exemplary assays that can be used to detect or measure ErbB3 in a sample include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence-activated cell sorting (FACS).

Samples that can be used in ErbB3 diagnostic assays according to the present invention include any tissue or fluid sample obtainable from a patient which contains detectable quantities of ErbB3 protein, or fragments thereof, under normal or pathological conditions. Generally, levels of ErbB3 in a particular sample obtained from a healthy patient (e.g., a patient not afflicted with a disease or condition associated with abnormal ErbB3 levels or activity) will be measured to initially establish a baseline, or standard, level of ErbB3. This baseline level of ErbB3 can then be com-

pared against the levels of ErbB3 measured in samples obtained from individuals suspected of having a ErbB3 related disease or condition.

EXAMPLES

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the methods and compositions of the invention, and are not intended to limit the scope of what the inventors regard as their invention. Efforts have been made to ensure accuracy with respect to numbers used (e.g., amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

Example 1

Generation of Human Antibodies to Human ErbB3

An immunogen comprising the ecto-domain of human ErbB3 was administered directly, with an adjuvant to stimulate the immune response, to a VELOCIMMUNE® mouse comprising DNA encoding human Immunoglobulin heavy and kappa light chain variable regions. The antibody immune response was monitored by a ErbB3-specific immunoassay. When a desired immune response was achieved splenocytes were harvested and fused with mouse myeloma cells to preserve their viability and form hybridoma cell lines. The hybridoma cell lines were screened and selected

to identify cell lines that produce ErbB3-specific antibodies. Using this technique several anti-ErbB3 chimeric antibodies (i.e., antibodies possessing human variable domains and mouse constant domains) were obtained; exemplary antibodies generated in this manner were designated as follows: H1M1819N, H2M1821N, H2M1824N, H2M1827N, H1M1828N, H2M1829N, H2M1930N, H2M1934N, H2M1936N, H2M1937N, H2M1938N, and H1M1940N.

Anti-ErbB3 antibodies were also isolated directly from antigen-positive B cells without fusion to myeloma cells, as described in US 2007/0280945A1. Using this method, several fully human anti-ErbB3 antibodies (i.e., antibodies possessing human variable domains and human constant domains) were obtained; exemplary antibodies generated in this manner were designated as follows: H4H2084P, H4H2092P, H4H2094P, H4H2098P, H4H2102P, H4H2108P, H4H2111P, H4H2114P, H4H2132P, H4H2138P, H4H2140P, H4H2143P, H4H2146P, H4H2147P, H4H2148P, H4H2151P, H4H2153P, H4H2154P, and H4H2290P.

Certain biological properties of the exemplary anti-ErbB3 antibodies generated in accordance with the methods of this Example are described in detail in the Examples set forth below.

Example 2

Heavy and Light Chain Variable Region Amino Acid Sequences

Table 1 sets forth the heavy and light chain variable region amino acid sequence pairs of selected anti-ErbB3 antibodies and their corresponding antibody identifiers.

TABLE 1

Antibody	SEQ ID NOS:							
	Designation	HCVR	HCDR1	HCDR2	HCDR3	LCVR	LCDR1	LCDR2
2084P	2	4	6	8	10	12	14	16
2092P	18	20	22	24	26	28	30	32
2094P	34	36	38	40	42	44	46	48
2098P	50	52	54	56	58	60	62	64
2102P	66	68	70	72	74	76	78	80
2108P	82	84	86	88	90	92	94	96
2111P	98	100	102	104	106	108	110	112
2114P	114	116	118	120	122	124	126	128
2132P	130	132	134	136	138	140	142	144
2138P	146	148	150	152	154	156	158	160
2140P	162	164	166	168	170	172	174	176
2143P	178	180	182	184	186	188	190	192
2146P	194	196	198	200	202	204	206	208
2147P	210	212	214	216	218	220	222	224
2148P	226	228	230	232	234	236	238	240
2151P	242	244	246	248	250	252	254	256
2153P	258	260	262	264	266	268	270	272
2154P	274	276	278	280	282	284	286	288
2290P	290	292	294	296	298	300	302	304
1819N	306	308	310	312	314	316	318	320
1821N	322	324	326	328	330	332	334	336
1824N	338	340	342	344	346	348	350	352
1827N	354	356	358	360	362	364	366	368
1828N	370	372	374	376	378	380	382	384
1829N	386	388	390	392	394	396	398	400
1930N	402	404	406	408	410	412	414	416
1934N	418	420	422	424	426	428	430	432
1936N	434	436	438	440	442	444	446	448
1937N	450	452	454	456	458	460	462	464
1938N	466	468	470	472	474	476	478	480
1940N	482	484	486	488	490	492	494	496

Antibodies are typically referred to herein according to the following nomenclature: Fc prefix (e.g. “H4H”, “H1M”, “H2M”), followed by a numerical identifier (e.g. “2084” as shown in Table 1), followed by a “P” or “N” suffix. Thus, according to this nomenclature, an antibody may be referred to herein as, e.g., “H4H2084P”. The H4H, H1M, and H2M prefixes on the antibody designations used herein indicate the particular Fc region of the antibody. For example, an “H2M” antibody has a mouse IgG2 Fc, whereas an “H4H” antibody has a human IgG4 Fc. As will be appreciated by a person of ordinary skill in the art, an H1M or H2M antibody can be converted to an H4H antibody, and vice versa, but in any event, the variable domains (including the CDRs)—which are indicated by the numerical identifiers shown in Table 1—will remain the same. The P and N suffixes on the antibody designations used herein refer to antibodies having heavy and light chains with identical CDR sequences but with sequence variations in regions that fall outside of the CDR sequences (i.e., in the framework regions). Thus, P and N variants of a particular antibody have identical CDR sequences within their heavy and light chain variable regions but differ from one another within their framework regions.

Control Constructs Used in the Following Examples

Various control constructs (anti-ErbB3 antibodies) were included in the following experiments for comparative purposes. The control constructs are designated as follows: Control I: a human anti-ErbB3 antibody with heavy and light chain variable domains having the amino acid sequences of the corresponding domains of “Mab#6,” as set forth in U.S. Pat. No. 7,846,440; Control II: a human

anti-ErbB3 antibody with heavy and light chain variable domains having the amino acid sequences of the corresponding domains of “U1-59,” as set forth in U.S. Pat. No. 7,705,130; and Control III: a human anti-ErbB3 antibody with heavy and light chain variable domains having the amino acid sequences of the corresponding domains of “U1-53,” as set forth in U.S. Pat. No. 7,705,130.

Example 3

Surface Plasmon Resonance Derived Binding Affinities and Kinetic Constants of Human Monoclonal Anti-ErbB3 Antibodies

Binding affinities and kinetic constants of human monoclonal anti-ErbB3 antibodies were determined by surface plasmon resonance at 25° C. and 37° C. (Tables 2-4). Measurements were conducted on a Biacore 2000 or T100 instrument. Antibodies, expressed with either mouse Fc (prefix H1M; H2M) or human IgG4 Fc (prefix H4H), were captured on an anti-mouse or anti human-Fc sensor surface (Mab capture format), and soluble monomeric (ErbB3.mmh; SEQ ID NO:497,) or dimeric (ErbB3-hFc; SEQ ID NO:498 or ErbB3-mFc; SEQ ID NO:499) protein was injected over the surface. Kinetic association (k_a) and dissociation (k_d) rate constants were determined by processing and fitting the data to a 1:1 binding model using Scrubber 2.0 curve fitting software. Binding dissociation equilibrium constants (K_D) and dissociative half-lives ($t_{1/2}$) were calculated from the kinetic rate constants as: $K_D(M) = k_d/k_a$; and $t_{1/2}(\text{min}) = (\ln 2 / (60 * k_d))$. Several clones showed sub-nanomolar affinity to monomeric (hErbB3.mmh) ErbB3 protein.

TABLE 2

Biacore Binding Affinities of Hybridoma mAbs (H1M and H2M) at 25° C. Binding at 25° C./Mab Capture Format					
Antibody	Analyte	k_a ($\text{M}^{-1}\text{s}^{-1}$)	k_d (s^{-1})	K_D (Molar)	$T_{1/2}$
H1M1819N	hErbB3.mmh	3.19E+05	3.22E-04	1.01E-09	36
	hErbB3.hFc	4.80E+05	5.88E-05	1.22E-10	196
H2M1821N	hErbB3.mmh	2.29E+05	1.99E-04	8.67E-10	58
	hErbB3.hFc	4.61E+05	1.90E-05	4.13E-11	608
H2M1824N	hErbB3.mmh	2.23E+05	4.56E-05	2.05E-10	254
	hErbB3.hFc	4.31E+05	1.44E-06	3.34E-12	8026
H2M1827N	hErbB3.mmh	2.19E+05	8.96E-05	4.09E-10	129
	hErbB3.hFc	4.39E+05	7.58E-06	1.73E-11	1524
H1M1828N	hErbB3.mmh	5.13E+05	2.65E-04	5.15E-10	44
	hErbB3.hFc	1.56E+06	4.34E-05	2.79E-11	266
H2M1829N	hErbB3.mmh	2.30E+05	6.46E-05	2.81E-10	179
	hErbB3.hFc	4.36E+05	8.61E-06	1.98E-11	1341
H2M1930N	hErbB3.mmh	1.96E+05	1.09E-04	5.59E-10	106
	hErbB3.hFc	4.04E+05	8.27E-06	2.05E-11	1396
H2M1934N	hErbB3.mmh	1.68E+05	7.35E-05	4.38E-10	157
	hErbB3.hFc	3.59E+05	7.97E-06	2.22E-11	1450
H2M1936N	hErbB3.mmh	4.32E+04	2.85E-04	6.59E-09	41
	hErbB3.hFc	6.41E+04	6.97E-05	1.09E-09	166
H2M1937N	hErbB3.mmh	8.26E+04	5.63E-05	6.82E-10	205
	hErbB3.hFc	1.10E+05	1.27E-05	1.16E-10	908
H2M1938N	hErbB3.mmh	2.41E+05	1.44E-04	5.99E-10	80
	hErbB3.hFc	4.51E+05	1.36E-05	3.01E-11	851
H1M1940N	hErbB3.mmh	2.89E+05	1.38E-04	4.77E-10	84
	hErbB3.hFc	4.60E+05	2.43E-05	5.29E-11	475
Control I	hErbB3.mmh	5.14E+04	2.15E-04	4.18E-09	54
	hErbB3.hFc	4.63E+04	1.63E-05	3.51E-10	711
Control II	hErbB3.mmh	1.41E+05	3.24E-04	2.30E-09	36
	hErbB3.hFc	1.53E+05	4.28E-05	2.80E-10	270
Control III	hErbB3.mmh	1.54E+06	3.15E-02	2.05E-08	0.4
	hErbB3.hFc	3.78E+06	8.84E-05	2.34E-11	131

TABLE 3

Biacore Binding Affinities of Human Fc mAbs (H4H) at 25° C. Binding at 25° C./Mab Capture Format					
Analyte		ka (Ms ⁻¹)	kd (s ⁻¹)	K _D (Molar)	T _{1/2}
H4H1819N	hErbB3.mmh	8.10E+06	3.51E-04	4.35E-11	33
	hErbB3.mFc	1.64E+07	1.54E-05	9.43E-13	748
H4H1821N	hErbB3.mmh	3.80E+06	1.92E-04	5.10E-11	60
	hErbB3.mFc	1.22E+07	4.33E-06	3.55E-13	2665
H4H2084P	hErbB3.mmh	2.49E+06	5.96E-05	2.39E-11	179
	hErbB3.mFc	3.83E+06	3.95E-06	1.03E-12	2695
H4H2092P	hErbB3.mmh	3.72E+06	1.03E-04	2.78E-11	103
	hErbB3.mFc	5.16E+06	7.46E-06	1.45E-12	1429
H4H2094P	hErbB3.mmh	1.89E+06	1.37E-05	7.22E-12	780
	hErbB3.mFc	3.03E+06	1.37E-06	4.52E-13	7779
H4H2098P	hErbB3.mmh	1.14E+06	7.89E-05	6.90E-11	135
	hErbB3.mFc	2.21E+06	8.97E-06	4.06E-12	1188
H4H2102P	hErbB3.mmh	8.86E+05	4.88E-05	5.51E-11	218
	hErbB3.mFc	1.58E+06	2.26E-06	1.43E-12	4721
H4H2108P	hErbB3.mmh	1.95E+06	8.13E-05	4.18E-11	131
	hErbB3.mFc	2.96E+06	4.33E-06	1.46E-12	2458
H4H2111P	hErbB3.mmh	2.21E+06	1.18E-04	5.31E-11	91
	hErbB3.mFc	3.50E+06	8.69E-06	2.49E-12	1225
H4H2114P	hErbB3.mmh	9.29E+05	9.88E-05	1.06E-10	108
	hErbB3.mFc	1.48E+06	7.98E-06	5.41E-12	1335
H4H2132P	hErbB3.mmh	2.16E+06	3.81E-05	1.77E-11	279
	hErbB3.mFc	3.49E+06	3.35E-06	9.58E-13	3183
H4H2138P	hErbB3.mmh	2.39E+06	5.01E-05	2.09E-11	213
	hErbB3.mFc	3.71E+06	5.46E-06	1.47E-12	1952
H4H2140P	hErbB3.mmh	1.66E+06	3.27E-05	1.98E-11	326
	hErbB3.mFc	2.51E+06	9.86E-07	3.93E-13	10797
H4H2143P	hErbB3.mmh	1.83E+06	9.73E-05	5.31E-11	109
	hErbB3.mFc	2.86E+06	4.63E-06	1.75E-12	2302
H4H2146P	hErbB3.mmh	2.79E+06	3.46E-05	1.24E-11	308
	hErbB3.mFc	4.54E+06	1.98E-06	4.35E-13	5392
H4H2147P	hErbB3.mmh	2.47E+06	1.08E-04	4.38E-11	98
	hErbB3.mFc	3.33E+06	4.58E-06	1.50E-12	2325
H4H2148P	hErbB3.mmh	3.98E+06	3.47E-05	8.71E-12	307
	hErbB3.mFc	5.91E+06	1.74E-06	2.95E-13	6110
H4H2151P	hErbB3.mmh	3.04E+06	2.86E-05	9.42E-12	372
	hErbB3.mFc	4.48E+06	9.52E-07	2.13E-13	11186
H4H2153P	hErbB3.mmh	2.94E+06	3.43E-05	1.17E-11	311
	hErbB3.mFc	3.67E+06	1.24E-06	3.37E-13	8603
H4H2154P	hErbB3.mmh	2.13E+06	3.73E-05	1.76E-11	285
	hErbB3.mFc	3.25E+06	9.77E-07	3.00E-13	10901
H4H2290P	hErbB3.mmh	5.82E+05	6.72E-05	1.15E-10	159
	hErbB3.mFc	8.00E+05	1.13E-05	1.40E-11	945

TABLE 4

Biacore Binding Affinities of Select mAbs at 37° C. Binding at 37° C./Mab Capture Format					
Analyte		ka (Ms ⁻¹)	kd (s ⁻¹)	K _D (Molar)	T _{1/2}
H4H1819N	hErbB3.mmh	1.21E+07	1.56E-03	1.29E-10	7
	hErbB3.mFc	3.68E+07	5.62E-05	1.53E-12	206
H4H1821N	hErbB3.mmh	6.49E+06	1.08E-03	1.67E-10	11
	hErbB3.mFc	1.87E+07	3.55E-05	1.89E-12	326
Control I	hErbB3.mmh	1.58E+05	5.48E-04	3.47E-09	21
	hErbB3.mFc	2.60E+05	1.01E-04	3.90E-10	114
Control II	hErbB3.mmh	3.23E+05	1.34E-03	4.13E-09	9
	hErbB3.mFc	1.44E+06	1.37E-04	9.50E-11	84
Control III	hErbB3.mmh	3.40E+06	7.90E-02	2.40E-08	0.1
	hErbB3.mFc	1.05E+07	1.77E-04	1.68E-11	65

As shown in Tables 2-4, many of the exemplary antibodies tested in this Example exhibited high affinity binding to ErbB3 that was superior or equivalent to the binding affini-

ties of the control antibodies tested. Of note, several of the anti-ErbB3 antibodies of the present invention exhibited sub-nanomolar affinity to monomeric (hErbB3.mmh) ErbB3 protein.

Example 4

Anti-ErbB3 Antibodies Block Neuregulin 1b Binding to Human ErbB3

To further characterize anti-hErbB3 mAbs of the present invention, their ability to block ligand binding was examined via ELISA. Plates were coated with neuregulin1 b (1 µg/ml) overnight and then antibodies (0-50 nM) were incubated (1 hr, 25° C.) with either 50 pM ErbB3-hFc (SEQ ID NO:498; for hybridomas) or 50 pM ErbB3-mFc (SEQ ID NO:499; for hIgG4 antibodies) and then added to coated plates and allowed to incubate for an additional 1 hr at 25° C. Plates were washed and non-sequestered (plate bound)

ErbB3 was detected with an anti-Fc poly conjugated with horseradish peroxidase (HRP). Plates were developed with TMB (3,3',5,5'-tetramethylbenzidine) and neutralized with sulfuric acid before reading absorbance at 450 nm on a Victor X5 plate reader. Data analysis used a sigmoidal dose-response model within Prism™ software. The calculated IC₅₀ value, defined as 50% of the antibody concentration required to achieve maximum blocking, was used as an indicator of blocking potency. Maximal blocking for each antibody was calculated by taking the difference in absorbance from zero to 50 nM antibody on the inhibition curve, divided by the difference in absorbance from 50 pM to zero ErbB3 on the dose curve. Results are shown in Tables 5 and 6.

TABLE 5

IC ₅₀ Values for Anti-ErbB3 Hybridoma mAbs (H1M and H2M)		
Antibody	IC50 (M)	Maximal Blocking (%)
H1M1819N	3.15E-11	92
H2M1821N	2.85E-11	96
H2M1824N	2.51E-11	99
H2M1827N	2.29E-11	98
H1M1828N	3.00E-11	95
H2M1829N	2.38E-11	98
H2M1930N	2.22E-11	87
H2M1934N	2.61E-11	80
H2M1936N	5.27E-10	91
H2M1937N	4.40E-11	95
H2M1938N	2.49E-11	85
H1M1940N	5.30E-10	80

TABLE 6

IC ₅₀ Values for Anti-ErbB3 Human Fc mAbs (H4H)		
Antibody	IC50 (M)	Maximal Blocking (%)
H4H1819N	2.00E-11	99
H4H1821N	1.80E-11	99
H4H2084P	8.73E-11	95
H4H2092P	5.94E-11	100
H4H2094P	9.00E-11	92
H4H2098P	1.35E-10	95
H4H2102P	1.86E-10	90
H4H2108P	1.16E-10	91

TABLE 6-continued

IC ₅₀ Values for Anti-ErbB3 Human Fc mAbs (H4H)		
Antibody	IC50 (M)	Maximal Blocking (%)
H4H2111P	4.97E-11	92
H4H2114P	1.63E-10	91
H4H2132P	9.57E-11	94
H4H2138P	1.06E-10	96
H4H2140P	9.46E-11	83
H4H2143P	8.35E-11	92
H4H2146P	1.77E-10	83
H4H2147P	5.06E-11	99
H4H2148P	5.08E-11	100
H4H2151P	7.51E-11	85
H4H2153P	7.40E-11	82
H4H2154P	9.01E-11	91
H4H2290P	6.64E-11	99
Control I	5.74E-10	98
Control III	8.32E-11	96

As shown in Tables 5 and 6, several anti-ErbB3 antibodies of the present invention showed potent blocking and had IC₅₀ values that were at the theoretical bottom (25 pM) of the assay.

Example 5

Anti-ErbB3 mAbs Effectively Internalize Cell Surface ErbB3

To determine if anti-ErbB3 mAbs effectively internalize cell surface bound ErbB3, MCF-7 cells were incubated with select anti-ErbB3 antibody (10 µg/ml) for 30 minutes on ice, washed and then stained with a Dylight 488 conjugated anti-human Fab (10 µg/ml) for 30 minutes on ice. Tubes were then washed and split between an on ice and 37° C. incubation for 1 hour. After incubation all tubes were placed on ice and a Dylight 488 quenching antibody (50 µg/ml) was added. Solutions were incubated an additional 1 hour on ice. Fluorescent signals were measured using an Accuri flow cytometer.

As a relative measure of the amount of ErbB3 that was internalized upon antibody binding and subsequent incubation at 37° C., the internalized mean fluorescent intensity (MFI) was calculated as follows: t,?

The calculation of QE (quenching efficiency) assumes that no internalization occurs at 4° C. Table 7 shows that all antibodies tested induce HERS internalization.

TABLE 7

Antibody-Induced HER3 Internalization at 37° C.				
Antibody	Total MFI mean ± S.D.	Surface MFI mean ± S.D.	Internalized MFI mean ± S.D.	% Internalized mean ± S.D.
H4H1819N	39233 ± 9261	22663 ± 5026	16570 ± 5329	42 ± 7
H4H1821N	32351 ± 5658	11607 ± 4781	20744 ± 4993	64 ± 14
Control I	19004 ± 5903	11598 ± 6602	7406 ± 1776	42 ± 20
Control II	41517 ± 5696	23540 ± 11994	17977 ± 6299	45 ± 21
Control III	27349 ± 5310	8010 ± 729	19338 ± 5934	69 ± 8

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Example 6

Inhibition of NRG1-Dependent Akt
Phosphorylation by Anti-ErbB3 Antibodies

Anti-ErbB3 antibodies were tested for their ability to inhibit phosphorylation of Akt in DU145 prostate cancer cells. Binding of NRG1 to ErbB3 results in ErbB3 phosphorylation, which leads to recruitment and activation of phosphatidylinositol 3-kinase (PI3-K). Activated PI3-K phosphorylates and activates the kinase Akt. Thus, Akt phosphorylation is a downstream marker of ErbB3 receptor activation. DU145 cells were seeded in 96-well plates and then serum-starved in medium containing 1% FBS overnight. Cells were then stimulated with 0.5 nM NRG1 (R&D Systems) for 30 min in the presence of 0.5 $\mu\text{g/ml}$ human Fc control protein or various anti-ErbB3 antibodies at concentrations of 0.01, 0.1 or 0.5 $\mu\text{g/ml}$. Each concentration of antibody was tested in triplicate. Cells were lysed and the relative levels of phosphorylated Akt were determined using a phospho-Akt cell-based ELISA kit (R&D Systems), according to the manufacturer's instructions. The average percent inhibition of Akt phosphorylation for each anti-ErbB3 antibody versus the Fc control group is shown in Table 8.

TABLE 8

Inhibition of Akt phosphorylation by Anti-ErbB3 Antibodies			
Antibody	Percent inhibition of Akt phosphorylation		
	0.01 $\mu\text{g/ml}$ ErbB3 antibody	0.1 $\mu\text{g/ml}$ ErbB3 antibody	0.5 $\mu\text{g/ml}$ ErbB3 antibody
H1M1819N	29	72	75
H2M1821N	11	68	73
H2M1824N	25	63	74
H2M1827N	16	73	75
H1M1828N	22	66	75
H2M1829N	22	74	74
H2M1930N	39	64	66
H2M1934N	20	56	67
H2M1936N	6	30	67
H2M1937N	-13	41	71
H2M1938N	40	63	74
H1M1940N	13	50	68
Control I	-1	46	60
Control II	4	7	51
Control III	3	45	55

This example illustrates that several of the anti-ErbB3 antibodies of the present invention exhibited more potent blockade of Akt phosphorylation than the control anti-ErbB3 antibodies. For example, antibodies H1M1819N, H2M1821N, H2M1824N, H2M1827N, H1M1828N, H2M1829N, H2M1930N and H2M1938N inhibited Akt phosphorylation by at least 60% at the 0.1 $\mu\text{g/ml}$ dose, while none of the control ErbB3 antibodies achieved an inhibition greater than 46% at that dose.

Example 7

Inhibition of Tumor Cell Growth by Anti-ErbB3
Antibodies

Select anti-ErbB3 antibodies were tested for their ability to inhibit the growth of A431 epidermoid carcinoma cells when used in combination with EGFR blockade. A431 cells in 96-well plates were incubated in medium containing 0.5% FBS and stimulated with 1 nM neuregulin-1 (NRG1) in the

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presence of an anti-EGFR antibody (1 $\mu\text{g/ml}$), an anti-ErbB3 antibody (1 $\mu\text{g/ml}$) or anti-EGFR (1 $\mu\text{g/ml}$) plus anti-ErbB3 antibody at 0.05, 0.25 or 1.0 $\mu\text{g/ml}$. The ligand (NRG1) and blocking antibodies (EGFR & ErbB3) were added at 0, 24 and 48 hrs during the 72-hour experiment. The relative change in the number of viable cells from the start of treatment until the 72-hour time point was reached was determined using standard methods (Cell Proliferation Assay Kit; Promega). The average percent decrease in cell growth for each anti-ErbB3 antibody versus an isotype control group is shown in Table 9.

TABLE 9

Inhibition of A431 Cell Growth by Anti-ErbB3 Antibodies				
Antibody	Percent decrease in the growth of A431 cells			
	1.0 $\mu\text{g/ml}$ ErbB3 antibody	anti-EGFR antibody + 0.05 $\mu\text{g/ml}$ ErbB3 antibody	anti-EGFR antibody + 0.25 $\mu\text{g/ml}$ ErbB3 antibody	anti-EGFR antibody + 1.0 $\mu\text{g/ml}$ ErbB3 antibody
H1M1819N	34	61	78	91
H2M1821N	16	35	62	85
H2M1824N	33	45	68	85
H2M1827N	15	53	75	84
H1M1828N	30	55	73	85
H2M1829N	31	53	76	89
H2M1930N	3	23	36	39
H2M1934N	-3	24	30	28
H2M1938N	5	37	56	60
H1M1940N	-4	19	20	19
Control I	19	31	37	56
Control III	7	22	21	32

This example illustrates that several of the anti-ErbB3 antibodies of the present invention exhibited more potent inhibition of A431 cell growth than the control anti-ErbB3 antibodies. For example, antibodies H1M1819N, H2M1821N, H2M1824N, H2M1827N, H1M1828N and H2M1829N inhibited cell growth by at least 60% at the 0.25 $\mu\text{g/ml}$ dose when combined with anti-EGFR antibody, while control antibodies I and III inhibited cell growth by only 37% and 21%, respectively, under these experimental conditions.

Example 8

Inhibition of ErbB3 and Akt Phosphorylation by
Anti-ErbB3 Antibodies

Select anti-ErbB3 antibodies were tested for their ability to inhibit NRG1-stimulated phosphorylation of ErbB3 and Akt in A431 epidermoid carcinoma and MCF7 breast cancer cells. In the first experiment, A431 cells were seeded in 6-well plates and incubated in complete medium overnight. Cells were then serum-starved (0.5% FBS) for 1 hr and stimulated with 1 nM NRG1 (R&D Systems) for 30 min in the presence of 5.0 $\mu\text{g/ml}$ of isotype control or anti-ErbB3 antibody at 0.05, 0.25 or 5.0 $\mu\text{g/ml}$. Cells were lysed and Western blots were performed using antibodies against ErbB3 and Akt as well as their phosphorylated forms using standard methods. The ratios of phosphorylated ErbB3 or Akt to total ErbB3 or Akt were calculated and used to determine the percent inhibition of Akt or ErbB3 phosphorylation for each of the anti-ErbB3 antibodies relative to isotype control. Results for the inhibition of ErbB3 or AKT phosphorylation in A431 cells are shown in Tables 10 and 11, respectively.

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TABLE 10

Percent Inhibition of ErbB3 Phosphorylation in A431 Cells			
Antibody	0.05 µg/ml	0.25 µg/ml	5.0 µg/ml
H4H1819N	98	105	107
H4H1821N	63	113	120
Control I	-11	14	72
Control III	-30	-9	-57

TABLE 11

Percent Inhibition of Akt Phosphorylation in A431 Cells			
Antibody	0.05 µg/ml	0.25 µg/ml	5.0 µg/ml
H4H1819N	84	104	113
H4H1821N	67	106	117
Control I	32	47	75
Control III	43	51	58

In a similar experiment, MCF7 cells were seeded in 6-well plates and incubated in complete medium for 2 days. Cells were then serum-starved (0.5% FBS) for 1 hr and then stimulated with 1 nM NRG1 (R&D Systems) for 30 min in the presence of 5.0 µg/ml of isotype control or anti-ErbB3 antibody at of 0.05, 0.25, 1.0 or 5.0 µg/ml. Western blots and data analysis were carried out in a similar manner for those experiments conducted with A431 cells. Results for the inhibition of ErbB3 or AKT phosphorylation in MCF7 cells are shown in Tables 12 and 13, respectively.

TABLE 12

Percent Inhibition of ErbB3 Phosphorylation in MCF7 Cells				
Antibody	0.05 µg/ml	0.25 µg/ml	1.0 µg/ml	5.0 µg/ml
H4H1819N	37	79	92	96
H4H1821N	57	92	96	97
Control I	0	17	44	81
Control III	4	12	60	61

TABLE 13

Percent Inhibition of Akt Phosphorylation in MCF7 Cells				
Antibody	0.05 µg/ml	0.25 µg/ml	1.0 µg/ml	5.0 µg/ml
H4H1819N	13	36	80	90
H4H1821N	17	69	82	89
Control I	21	29	34	46
Control III	35	28	29	35

This Example illustrates that representative anti-ErbB3 antibodies of the invention exhibited superior ability to inhibit phosphorylation of ErbB3 and Akt compared to control antibodies under most of the experimental conditions tested. In A431 cells, for example, H4H1819N and H4H1821N completely inhibited both ErbB3 and Akt phosphorylation at 0.25 µg/ml while the control antibodies never achieved complete inhibition, even at 5.0 µg/ml. Similarly, in MCF7 cells, H4H1819N and H4H1821N at 1.0 µg/ml inhibited ErbB3 and Akt phosphorylation to a greater extent than either of the control anti-ErbB3 antibodies even at 5.0 µg/ml.

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Example 9

Inhibition of Tumor Growth by Anti-ErbB3 Antibodies

Select anti-ErbB3 antibodies were tested for their ability to inhibit the growth of human tumor xenografts in immunocompromised mice. Briefly, $1-5 \times 10^6$ A431 human epidermoid carcinoma cells or A549 human non-small cell lung cancer cells (ATCC) were implanted subcutaneously into the flank of 6-8 week old SCID mice (Taconic, Hudson, N.Y.). After tumors reached an average volume of 100-150 mm³, mice were randomized into groups for treatment (n=6 mice per group). In the first experiment, mice bearing A431 tumors were administered human Fc (SEQ ID NO:500, 12.5 mg/kg), or anti-ErbB3 antibody (0.5 or 12.5 mg/kg). All antibodies were administered via subcutaneous injection twice per week for approximately 3 weeks. Tumor volumes were measured twice per week over the course of the experiment and tumor weights were determined upon excision of tumors at the conclusion of the experiment. Average tumor size relative to the Fc treated group as well as final tumor weights were calculated for each group. Results are summarized in Table 14.

TABLE 14

Inhibition of A431 Tumor Growth in SCID Mice (Hybridoma mAbs - H1M and H2M)				
Antibody (mg/kg)	Tumor Growth in mm ³ from Start of Treatment (mean ± S.D.)	Average % Decrease in Tumor Growth	Avg Tumor Weight (g)	Average % Decrease in Tumor Weight
hFc ctrl (12.5)	860 ± 358	—	0.778 ± 0.268	—
H1M1819N (0.5)	355 ± 178	59	0.520 ± 0.155	33
H2M1821N (0.5)	280 ± 131	67	0.428 ± 0.209	45
H2M1827N (0.5)	246 ± 71	71	0.432 ± 0.152	45
H2M1829N (0.5)	392 ± 265	54	0.480 ± 0.283	38
Control I (0.5)	862 ± 199	0	0.815 ± 0.190	-5
Control I (12.5)	299 ± 139	65	0.438 ± 0.217	44

In a similar experiment, using selected antibodies in the human IgG4 format yield similar results, as summarized in Table 15.

TABLE 15

Inhibition of A431 Tumor Growth in SCID Mice (Human Fc mAbs - H4H)				
Antibody (mg/kg)	Tumor Growth in mm ³ from Start of Treatment (mean ± S.D.)	Average % Decrease in Tumor Growth	Avg Tumor Weight (g)	Average % Decrease in Tumor Weight
hFc ctrl (12.5)	797 ± 65	—	1.31 ± 0.142	—
H4H1819N (0.5)	161 ± 69	80	0.453 ± 0.010	65
H4H1819N (12.5)	110 ± 47	86	0.458 ± 0.108	65
H4H1821N (0.5)	148 ± 73	81	0.482 ± 0.058	63
H4H1821N (12.5)	74 ± 100	91	0.392 ± 0.117	70
Control I (0.5)	675 ± 228	15	0.928 ± 0.215	29
Control I (12.5)	95 ± 51	88	0.361 ± 0.063	72

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TABLE 15-continued

Inhibition of A431 Tumor Growth in SCID Mice (Human Fc mAbs - H4H)				
Antibody (mg/kg)	Tumor Growth in mm ³ from Start of Treatment (mean ± S.D.)	Average % Decrease in Tumor Growth	Avg Tumor Weight (g)	Average % Decrease in Tumor Weight
Control III (0.5)	409 ± 254	49	0.687 ± 0.269	48
Control III (12.5)	219 ± 129	73	0.545 ± 0.096	58

In similar experiments, the effect of various anti-ErbB3 antibodies on the growth of A549 tumor xenografts was determined, as summarized in Table 16.

TABLE 16

Inhibition of A549 Tumor Growth in SCID Mice				
Antibody (mg/kg)	Tumor Growth in mm ³ from Start of Treatment (mean ± S.D.)	Average % Decrease in Tumor Growth	Avg Tumor Weight (g)	Average % Decrease in Tumor Weight
hFc ctrl (12.5)	727 ± 184	—	1.27 ± 0.332	—
H4H1821N (0.2)	366 ± 90	50	0.811 ± 0.145	37
H4H1821N (0.5)	347 ± 52	52	0.820 ± 0.245	36
H4H1821N (2.5)	346 ± 106	52	0.783 ± 0.175	39
Control I (0.5)	719 ± 230	1	1.328 ± 0.363	-3.78
Control I (2.5)	614 ± 177	15	0.985 ± 0.198	23

As shown in this Example, antibodies H4H1819N and H4H1821N each significantly inhibited tumor growth in vivo to an extent that was superior, or equivalent to the extent of tumor growth inhibition observed with administration of the control anti-ErbB3 antibodies tested.

Example 10

Inhibition of Tumor Growth by Anti-ErbB3 Antibodies in Combination with Agents that Block Other ErbB Family Members

The effect of a combination treatment with H4H1821N plus an inhibitory anti-EGFR antibody (“anti-EGFR mAb”) on human tumor xenograft growth was tested. Briefly, 2×10⁶ FaDu human hypopharyngeal carcinoma cells (ATCC) were implanted subcutaneously into the flank of 6-8 week old SCID mice (Taconic, Hudson, N.Y.). After tumors reached an average volume of 150-200 mm³, mice were randomized into groups for treatment (n=6 mice per group). Mice were administered human Fc control protein (12.5 mg/kg), H4H1821N (2.5 mg/kg), anti-EGFR mAb (10 mg/kg) or the combination of H4H1821N plus anti-EGFR mAb (2.5+10 mg/kg). All antibodies were administered via subcutaneous injection twice per week. Tumor volumes were measured twice per week over the course of the experiment and tumor weights were determined upon excision of tumors at the conclusion of the experiment. Averages (mean±/–standard deviation) of the tumor growth from the start of treatment and the tumor weights were calculated for each treatment group. The percent decrease of tumor growth and tumor

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weight was calculated from comparison to the Fc control group. The results are shown in Table 17.

TABLE 17

Inhibition of FaDu tumor xenograft growth in SCID mice				
Antibody (mg/kg)	Tumor Growth in mm ³ from Start of Treatment (mean ± S.D.)	Average % Decrease in Tumor Growth	Avg Tumor Weight (g)	Average % Decrease in Tumor Weight
hFc control (12.5)	1099 ± 186	—	0.993 ± 0.176	—
H4H1821N (2.5)	284 ± 175	74	0.522 ± 0.177	47
anti-EGFR mAb (10)	55 ± 115	95	0.215 ± 0.120	78
H4H1821N + anti-EGFR mAb (2.5 + 10)	-199 ± 38	118	0.024 ± 0.020	98

In a similar experiment, the effect of a combination treatment with H4H1821N plus the inhibitory anti-HER2 antibody clone 4D5v8 as described in Carter et al., *Proc. Natl. Acad. Sci. USA* 89:4285-4289 (1992) on human tumor xenograft growth was tested. Briefly, 1×10⁷ BT474 human breast cancer cells (ATCC) were implanted subcutaneously into the flank of 6-8 week old NCR nude mice (Taconic, Hudson, N.Y.). After tumors reached an average volume of 150-200 mm³, mice were randomized into groups for treatment (n=5 mice per group). Mice were administered human Fc control protein (25 mg/kg), H4H1821N (12.5 mg/kg), 4D5v8 (12.5 mg/kg) or the combination of H4H1821N plus 4D5v8 (12.5+12.5 mg/kg). All antibodies were administered via subcutaneous injection twice per week. Tumor volumes were measured twice per week over the course of the experiment. The average (mean±/–standard deviation) tumor growth from the start of treatment was calculated for each treatment group. The percent decrease of tumor growth was calculated from comparison to the Fc control group. The results are shown in Table 18.

TABLE 18

Inhibition of BT474 tumor xenograft growth in nude mice		
Antibody (mg/kg)	Tumor growth in mm ³ from start of treatment (mean ± SD)	Average % Decrease in Tumor Growth
hFc control (25)	194 ± 39	—
H4H1821N (12.5)	137 ± 65	29
4D5v8 (12.5)	34 ± 121	82
H4H1821N + 4D5v8 (12.5 + 12.5)	-79 ± 39	141

This example illustrates that combined treatment with H4H1821N plus anti-EGFR or anti-HER2 antibodies provides more potent inhibition of tumor growth than the single agent treatments. In both FaDu and BT474 tumor xenografts, the combination treatments, but not the single agents, caused the average tumor size to decrease (tumor regression).

Example 11

Epitope Mapping of H4H1821N Binding to ErbB3 by H/D Exchange

Experiments were conducted to determine the amino acid residues of ErbB3 with which H4H1821N interacts. For this

purpose H/D exchange epitope mapping was carried out. A general description of the H/D exchange method is set forth in e.g., Ehring (1999) Analytical Biochemistry 267(2):252-259; and Engen and Smith (2001) Anal. Chem. 73:256A-265A.

To map the binding epitope(s) of antibody H4H1821N on ErbB3 via H/D exchange, a recombinant construct consisting of the extracellular domain of hErbB3 (amino acids 1-613 of SEQ ID NO:498) with a C-terminal myc-myc-hexahistidine tag ("hErbB3-mmH") was used. hErbB3-mmH was first deglycosylated with PNGase F (New England BioLabs) under native conditions. Antibody H4H1821N was covalently attached to N-hydroxysuccinimide (NHS) agarose beads (GE Lifescience).

In the 'on-solution/off-beads' experiment (on-exchange in solution followed by off-exchange on beads), the ligand (deglycosylated hErbB3-mmH) was deuterated for 5 min or 10 min in PBS buffer prepared with D₂O, and then bound to H4H1821N beads through a 2 min incubation. The ErbB3-bound beads were washed with PBS aqueous buffer (prepared with H₂O) and incubated for half of the on-exchange time in PBS buffer. After the off-exchange, the bound ErbB3 was eluted from beads with an ice-cold low pH TFA solution. The eluted ErbB3 was then digested with immobilized pepsin (Thermo Scientific) for 5 min. The resulting peptides were desalted using ZipTip® chromatographic pipette tips and immediately analyzed by UltrafleXtreme matrix assisted laser desorption ionization time of flight (MALDI-TOF) mass spectrometry (MS).

In the 'on-beads/off-beads' experiment (on-exchange on beads followed by off-exchange on beads), ErbB3 was first bound to H4H1821N beads and then incubated for 5 min or 10 min in D₂O for on-exchange. The following steps (off-exchange, pepsin digestion, and MS analysis) were carried out as described for the 'on-solution/off-beads' procedure. The centroid values or average mass-to-charge ratios (m/z) of all the detected peptides were calculated and compared between these two sets of experiments.

The results are summarized in Table 19 which provides a comparison of the centroid m/z values for all the detected peptides identified by liquid chromatography-matrix assisted laser desorption ionization (LC-MALDI) MS following the H/D exchange and peptic digest procedure. While the majority of the observed peptic peptides gave similar centroid values for both the on-solution/off-beads and on-beads/off-beads experiments, three segments corresponding to residues 345-367, 423-439, and 451-463 of the extracellular domain of ErbB3 (SEQ ID NO:498) had delta centroid values (Δ) greater than or equal to 0.20 m/z in both the '5 min on-/2.5 min off-exchange' experiment (Experiment I) and the '10 min on-/5 min off-exchange' experiment (Experiment II). For purposes of the present Example, a positive difference (Δ) of at least 0.20 m/z in both experiments indicates amino acids protected by antibody binding. Segments meeting this criterion are indicated by bold text and an asterisk (*) in Table 19.

TABLE 19

H4H1821N Binding to hErbB3-mmH						
Residues	Experiment I 5 min on-/2.5 min off-exchange			Experiment II 10 min on-/5 min off-exchange		
	(of SEQ ID NO: 498)	On- solution/ Off Beads	On-Beads/ Off- Beads	Δ	On- solution/ Off Beads	On-Beads/ Off- Beads
46-57	1287.52	1287.41	0.11	1287.58	1287.64	-0.06
58-63	844.97	844.97	0.00	845.04	844.99	0.06

TABLE 19-continued

H4H1821N Binding to hErbB3-mmH						
Residues	Experiment I 5 min on-/2.5 min off-exchange			Experiment II 10 min on-/5 min off-exchange		
	(of SEQ ID NO: 498)	On- solution/ Off Beads	On-Beads/ Off- Beads	Δ	On- solution/ Off Beads	On-Beads/ Off- Beads
58-66	1102.34	1102.25	0.09	1102.25	1102.30	-0.05
58-67	1265.65	1265.60	0.05	1265.57	1265.50	0.07
58-69	1477.84	1477.77	0.07	1477.79	1477.79	0.01
59-69	1364.46	1364.48	-0.02	1364.39	1364.42	-0.03
61-69	1050.70	1050.67	0.03	1050.75	1050.68	0.07
75-96	2509.35	2509.27	0.08	2509.21	2509.21	0.01
76-96	2362.11	2362.09	0.01	2362.11	2361.97	0.14
84-96	1526.22	1526.05	0.16	1526.09	1526.08	0.01
84-98	1710.14	1710.11	0.03	1710.17	1710.07	0.11
84-99	1857.37	1857.34	0.03	1857.39	1857.33	0.06
86-96	1270.52	1270.50	0.02	1270.50	1270.45	0.05
100-114	1750.75	1750.60	0.15	1750.85	1750.75	0.11
100-114	1766.52	1766.55	-0.03	1766.63	1766.47	0.16
100-120	2476.03	2475.80	0.23	2476.04	2475.96	0.08
103-117	1789.63	1789.48	0.14	1789.69	1789.44	0.24
112-120	1142.00	1141.95	0.05	1142.01	1142.06	-0.05
144-154	1431.72	1431.72	0.00	1431.76	1431.67	0.08
345-365	2328.64	2328.64	0.00	2328.57	2328.64	-0.07
345-367*	2542.60	2542.34	0.26	2542.67	2542.47	0.20
366-378	1568.81	1568.70	0.11	1568.88	1568.78	0.10
368-373	807.97	807.95	0.02	807.94	807.88	0.06
368-376	1079.25	1079.30	-0.04	1079.38	1079.30	0.08
368-377	1242.49	1242.40	0.09	1242.48	1242.43	0.05
368-378	1355.82	1355.68	0.14	1355.70	1355.73	-0.03
368-379	1469.55	1469.56	-0.01	1469.63	1469.57	0.06
368-380	1583.09	1583.10	-0.01	1583.04	1583.03	0.01
369-378	1208.29	1208.25	0.03	1208.33	1208.30	0.03
397-408	1295.45	1295.47	-0.01	1295.41	1295.36	0.05
397-411	1643.12	1643.04	0.08	1643.03	1642.98	0.05
397-412	1756.26	1756.08	0.18	1756.18	1756.04	0.14
405-411	857.06	856.97	0.09	857.09	857.02	0.07
423-435	1434.94	1434.82	0.11	1434.96	1434.78	0.18
423-436*	1598.08	1597.89	0.20	1598.27	1598.06	0.21
424-439*	1812.55	1812.27	0.28	1812.76	1812.37	0.39
423-439*	1869.57	1869.29	0.28	1869.79	1869.41	0.38
424-435	1377.85	1377.69	0.16	1378.16	1377.93	0.22
424-436*	1541.12	1540.90	0.21	1541.20	1541.00	0.20
425-439*	1665.29	1665.04	0.26	1665.55	1665.22	0.33
451-463*	1585.74	1585.51	0.23	1585.77	1585.53	0.24
618-641	2828.04	2827.98	0.06	2827.98	2827.89	0.10
621-629	989.16	989.14	0.02	989.27	989.28	-0.01
621-641	2498.60	2498.59	0.01	2498.65	2498.53	0.12

The H/D exchange results summarized in Table 19 indicate that the three regions corresponding to amino acids 345-367, 423-439, and 451-463 of SEQ ID NO:498 are protected from full off-exchange by H4H1821N binding to ErbB3 after on-exchange. Significantly, all three regions are located within domain III of the ErbB3 extracellular domain. Therefore, this Example suggests that antibody H4H1821N binds a discontinuous epitope within domain III of the human ErbB3 extracellular domain consisting of these three amino acid segments or otherwise results in protection of these residues from H/D exchange (e.g., via conformational change or allosteric effects upon antibody binding).

Example 12

Clinical Trial of an Anti-ErbB3 Antibody in Combination with Erlotinib or Cetuximab in Patients with Advanced Colorectal Cancer (CRC), Non-Small Cell Lung Cancer (NSCLC) or Head and Neck Cancer (SCCHN)

A clinical trial is conducted with the exemplary anti-ErbB3 antibody H4H1821N in patients with advanced colorectal cancer (CRC), non-small cell lung cancer (NSCLC) or head and neck cancer (SCCHN). The trial is divided into two phases: a dose escalation phase and a safety expansion phase. In the dose escalation phase, all patients are initially administered H4H1821N intravenously (IV) at a dose of 3, 10 or 20 mg/kg. Following the initial dose of H4H1821N, the treatment regimen is modified based on cancer type: NSCLC patients begin a regimen of 150 mg Erlotinib once daily in combination with H4H1821N at 3, 10 or 20 mg/kg IV, once every 14 days; CRC and SCCHN patients begin a regimen of Cetuximab 250 mg/m² IV once a week in

combination with H4H1821N at 3, 10 or 20 mg/kg IV, once every 14 days. In the safety expansion phase, NSCLC patients receive H4H1821N (at the recommended Phase 2 dose) IV once every 14 days in combination with 150 mg Erlotinib once daily; CRC and SCCHN patients receive H4H1821N (at the recommended Phase 2 dose) IV once every 14 days in combination with Cetuximab 250 mg/m² IV once a week.

It is expected that combination therapy comprising the anti-ErbB3 antibody H4H1821N and Erlotinib or Cetuximab will provide observable clinical improvements in patients with NSCLC, CRC and/or SCCHN to a greater extent than monotreatment with Erlotinib or Cetuximab alone.

The present invention is not to be limited in scope by the specific embodiments describe herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and the accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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caggtgcagc tgggtggagtc tgggggaggc gtggtccagt ctgggaagtc cctgagactc      60
tcctgtgtag cgtctggatt caccttcagt aattatggca tgcactgggt ccgccagact      120
ccaggcaagg ggctggagtg ggtggcacgt atatggtttg atggaactaa taaatactac      180
acagactccg tgaagggccg attcacctg tccagagaca gttccaagaa cacgctgtat      240
ctgcaaatga acagcctgag agccgaggac acggctgtct atttctgtgc gagagaagag      300
tcattggaac tagaccacta tgttatggac gtctggggcc aagggaccac ggtcaccgtc      360
tcctca                                          366
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<210> SEQ ID NO 2

<211> LENGTH: 122

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 2

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Ser Gly Lys
 1           5           10           15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr
          20           25           30
Gly Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45
Ala Arg Ile Trp Phe Asp Gly Thr Asn Lys Tyr Tyr Thr Asp Ser Val
          50           55           60
Lys Gly Arg Phe Thr Leu Ser Arg Asp Ser Ser Lys Asn Thr Leu Tyr
          65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
```

-continued

85	90	95	
Ala Arg Glu Glu Ser Leu Glu Leu Asp His Tyr Val Met Asp Val Trp			
100	105	110	
Gly Gln Gly Thr Thr Val Thr Val Ser Ser			
115	120		

<210> SEQ ID NO 3
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 3

ggattcacct tcagtaatta tggc 24

<210> SEQ ID NO 4
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 4

Gly Phe Thr Phe Ser Asn Tyr Gly
 1 5

<210> SEQ ID NO 5
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 5

atatggtttg atggaactaa taaa 24

<210> SEQ ID NO 6
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 6

Ile Trp Phe Asp Gly Thr Asn Lys
 1 5

<210> SEQ ID NO 7
 <211> LENGTH: 45
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 7

gcgagagaag agtcattgga actagaccac tatggtatgg acgtc 45

<210> SEQ ID NO 8
 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 8

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Ala Arg Glu Glu Ser Leu Glu Leu Asp His Tyr Val Met Asp Val
 1 5 10 15

<210> SEQ ID NO 9
 <211> LENGTH: 324
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 9

gccatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca ggacattaga gatgatttag gctggtttca gcagaaaccc 120
 gggaaagccc ctaacctcct gatctatgct gcatccagtt taaaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tggcacagat ttcactctca ccatcagcag cctgcagcct 240
 gaggattttg caacttatta ctgtctacaa gattacaatt atccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa acga 324

<210> SEQ ID NO 10
 <211> LENGTH: 108
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 10

Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asp Asp
 20 25 30
 Leu Gly Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asn Tyr Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> SEQ ID NO 11
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 11

caggacatta gagatgat 18

<210> SEQ ID NO 12
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 12

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Gln Asp Ile Arg Asp Asp
1 5

<210> SEQ ID NO 13
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 13

gctgcatcc

9

<210> SEQ ID NO 14
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 14

Ala Ala Ser
1

<210> SEQ ID NO 15
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 15

ctacaagatt acaattatcc gctcact

27

<210> SEQ ID NO 16
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 16

Leu Gln Asp Tyr Asn Tyr Pro Leu Thr
1 5

<210> SEQ ID NO 17
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 17

gaggtgcagc tgggtggagtc tgggggaggt gtggtacggc ctgggggggtc cctgagactc 60

tctctgtcag cctctggatt cacctttgaa gattatggca tgaattgggt ccgccaagtt 120

ccaggggaagg ggctggagtg ggtctctggt actaattgga atggtggtat cacaggttat 180

acaggctctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctatat 240

ctacaaatga acagtctgag agccgaggac acggccttgt atcactgtgc gagagatagc 300

ggggatcaag atgcttttga tatctggggc caagggacaa tggtcaccgt ctcttca 357

<210> SEQ ID NO 18
<211> LENGTH: 119
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 18

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Tyr
 20 25 30
 Gly Met Asn Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Thr Asn Trp Asn Gly Gly Ile Thr Gly Tyr Thr Gly Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
 85 90 95
 Ala Arg Asp Ser Gly Asp Gln Asp Ala Phe Asp Ile Trp Gly Gln Gly
 100 105 110
 Thr Met Val Thr Val Ser Ser
 115

<210> SEQ ID NO 19
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 19

ggattcacct ttgaagatta tggc

24

<210> SEQ ID NO 20
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 20

Gly Phe Thr Phe Glu Asp Tyr Gly
 1 5

<210> SEQ ID NO 21
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 21

actaattgga atggtggtat caca

24

<210> SEQ ID NO 22
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 22

Thr Asn Trp Asn Gly Gly Ile Thr
 1 5

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<210> SEQ ID NO 23
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 23

gcgagagata gcggggatca agatgctttt gatatc 36

<210> SEQ ID NO 24
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 24

Ala Arg Asp Ser Gly Asp Gln Asp Ala Phe Asp Ile
 1 5 10

<210> SEQ ID NO 25
 <211> LENGTH: 324
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 25

gacatccagt tgaccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgct gggccagtc ggacattagc agttatttag cctggtatca gcaaaaacca 120
 gggaaagccc ctaaactcct gatctatgct gcatccactt tccaaagtgg ggtcccatca 180
 agattcagcg gcagtggatc tgggacagaa ttcactctca caatcagcaa cctgcagcct 240
 gaagattttg caacttatta ctgtcaacag cttgatagtt accctctctc tttcggcgga 300
 gggaccaagg tggagatcaa acga 324

<210> SEQ ID NO 26
 <211> LENGTH: 108
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 26

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Asp Ile Ser Ser Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Thr Phe Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asp Ser Tyr Pro Leu
 85 90 95
 Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105

-continued

<210> SEQ ID NO 27
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 27

caggacatta gcagttat

18

<210> SEQ ID NO 28
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 28

Gln Asp Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 29
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 29

gctgcatcc

9

<210> SEQ ID NO 30
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 30

Ala Ala Ser
1

<210> SEQ ID NO 31
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 31

caacagcttg atagttacc tctctct

27

<210> SEQ ID NO 32
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 32

Gln Gln Leu Asp Ser Tyr Pro Leu Ser
1 5

<210> SEQ ID NO 33
<211> LENGTH: 369
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 33

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gaggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc    60
tcctgtgcag cctctggatt cacctttagt agctacgaca tgcactgggt ccgccaagca    120
acaggaaaag gtctggagtg ggtctcagct attggctctg ctggtgacac atactatcca    180
gtctccgga tgggccgatt caccatctcc agagatgatg ccaagaactc cttgtatctt    240
caaatgaaca gcctgagagc cggggacacg gctgtctatt actgtgcaag agaggggggtc    300
acaattcgtc cggacgacta ctttggctctg gacgtctggg gccaaaggaac cacggtcacc    360
gtctccgcc                                     369
  
```

<210> SEQ ID NO 34
 <211> LENGTH: 123
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 34

```

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
  1           5           10
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
          20           25           30
Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val
          35           40           45
Ser Ala Ile Gly Pro Ala Gly Asp Thr Tyr Tyr Pro Val Ser Ala Met
          50           55           60
Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr Leu
  65           70           75           80
Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Ala
          85           90           95
Arg Glu Gly Val Thr Ile Arg Pro Asp Asp Tyr Phe Gly Leu Asp Val
          100          105          110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ala
          115          120
  
```

<210> SEQ ID NO 35
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 35

```

ggattcacct ttagtagcta cgac                                     24
  
```

<210> SEQ ID NO 36
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 36

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Gly Phe Thr Phe Ser Ser Tyr Asp
  1           5
  
```

-continued

<210> SEQ ID NO 37
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 37

attggtcctg ctggtgacac a 21

<210> SEQ ID NO 38
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 38

Ile Gly Pro Ala Gly Asp Thr
 1 5

<210> SEQ ID NO 39
 <211> LENGTH: 51
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 39

gcaagagagg gggtcacaat tcgtccggac gactactttg gtctggacgt c 51

<210> SEQ ID NO 40
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 40

Ala Arg Glu Gly Val Thr Ile Arg Pro Asp Asp Tyr Phe Gly Leu Asp
 1 5 10 15

Val

<210> SEQ ID NO 41
 <211> LENGTH: 324
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 41

gacatccagt tgaccagtc tccatccttc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgct gggccagtc gggcattagc gattatttag cctgggatca gaaaaaacca 120

gggaaagccc ctcagctcct gatctatgct gcaaccactt tgcaaagtgg ggtcccatct 180

aggttcagcg gcagtgatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagatthtg caacttatta ctgtcaacag ctttaactt acccactcac ttctggcgga 300

gggaccaagg tggagatcaa acga 324

<210> SEQ ID NO 42
 <211> LENGTH: 108
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 42

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Asp Tyr
 20 25 30

Leu Ala Trp Tyr Gln Lys Lys Pro Gly Lys Ala Pro Gln Leu Leu Ile
 35 40 45

Tyr Ala Ala Thr Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Thr Tyr Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> SEQ ID NO 43
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 43

cagggcatta gcgattat

18

<210> SEQ ID NO 44
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 44

Gln Gly Ile Ser Asp Tyr
 1 5

<210> SEQ ID NO 45
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 45

gctgcaacc

9

<210> SEQ ID NO 46
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 46

Ala Ala Thr
 1

<210> SEQ ID NO 47
 <211> LENGTH: 27

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<212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 47

caacagctta atacttacc actcact

27

<210> SEQ ID NO 48
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 48

Gln Gln Leu Asn Thr Tyr Pro Leu Thr
 1 5

<210> SEQ ID NO 49
 <211> LENGTH: 360
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 49

cagggtgcagc tgggtggagtc tgggggagggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag cgtctggatt caccttcagt agctttggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatggtatg ttgaaattaa taaataccat 180
 gcagactccg tgaagggccg attcaccatc tccagagacg attccaagaa cacggtatat 240
 ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagactgg 300
 aacgacgggg actacggtat ggacgtctgg ggccaagggg ccacggtcac cgtctcctca 360

<210> SEQ ID NO 50
 <211> LENGTH: 120
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 50

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Trp Tyr Val Glu Ile Asn Lys Tyr His Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Trp Asn Asp Gly Asp Tyr Gly Met Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

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<210> SEQ ID NO 51
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 51

ggattcacct tcagtagctt tggc

24

<210> SEQ ID NO 52
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 52

Gly Phe Thr Phe Ser Ser Phe Gly
 1 5

<210> SEQ ID NO 53
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 53

atatggtatg ttgaaattaa taaa

24

<210> SEQ ID NO 54
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 54

Ile Trp Tyr Val Glu Ile Asn Lys
 1 5

<210> SEQ ID NO 55
 <211> LENGTH: 39
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 55

gcgagagact ggaacgacgg ggactacggt atggacgtc

39

<210> SEQ ID NO 56
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 56

Ala Arg Asp Trp Asn Asp Gly Asp Tyr Gly Met Asp Val
 1 5 10

<210> SEQ ID NO 57
 <211> LENGTH: 324
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 57

```

gacatccagt tgaccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc      60
atcacttgct gggccagtc gggcattagc agtttttag cctggatca gcaaaaagca      120
gggaaagccc cgaggctcct gatctatgct gcatccactt tgcaaactgg ggtcccatca      180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct      240
ggagattttg caacttatca ctgtcaacag cttaatagtt acccgtacac ttttggccag      300
gggaccaagc tggagatcaa acga                                           324

```

<210> SEQ ID NO 58

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 58

```

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1           5           10           15
Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Ser Phe
          20           25           30
Leu Ala Trp Tyr Gln Gln Lys Ala Gly Lys Ala Pro Arg Leu Leu Ile
          35           40           45
Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
          50           55           60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
          65           70           75           80
Gly Asp Phe Ala Thr Tyr His Cys Gln Gln Leu Asn Ser Tyr Pro Tyr
          85           90           95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
          100           105

```

<210> SEQ ID NO 59

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 59

```

cagggcatta gcagtttt                                           18

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<210> SEQ ID NO 60

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 60

```

Gln Gly Ile Ser Ser Phe
 1           5

```

<210> SEQ ID NO 61

<211> LENGTH: 9

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 61

gctgcatcc

9

<210> SEQ ID NO 62

<211> LENGTH: 3

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 62

Ala Ala Ser

1

<210> SEQ ID NO 63

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 63

caacagctta atagttacc gtacact

27

<210> SEQ ID NO 64

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 64

Gln Gln Leu Asn Ser Tyr Pro Tyr Thr

1

5

<210> SEQ ID NO 65

<211> LENGTH: 369

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 65

gaggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tctctgtcag cctctggatt caccttcagt aactacgaca tacactgggt ccgccaagct 120

acaggaaaag gtctggagtg ggtctcagct attggtcctg ctggtgacac atactattca 180

gactccgtaa agggccgatt caccatctcc agagaagatg ccaagaactc cttgtatctt 240

caaatgagca gcctgagagc cggggacacg gctgtttatt actgtgcaag cgaggggata 300

gcagttcgtc cggacgacta ctacggtatg gacgtctggg gccaaaggac cacggtcacc 360

gtctccgcc 369

<210> SEQ ID NO 66

<211> LENGTH: 123

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 66

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

-continued

1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr	20	25	30
Asp Ile His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val	35	40	45
Ser Ala Ile Gly Pro Ala Gly Asp Thr Tyr Tyr Ser Asp Ser Val Lys	50	55	60
Gly Arg Phe Thr Ile Ser Arg Glu Asp Ala Lys Asn Ser Leu Tyr Leu	65	70	75
Gln Met Ser Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Ala	85	90	95
Ser Glu Gly Ile Ala Val Arg Pro Asp Asp Tyr Tyr Gly Met Asp Val	100	105	110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ala	115	120	

<210> SEQ ID NO 67
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 67

ggattcacct tcagtaacta cgac

24

<210> SEQ ID NO 68
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 68

Gly Phe Thr Phe Ser Asn Tyr Asp
1 5

<210> SEQ ID NO 69
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 69

attggtcctg ctggtgacac a

21

<210> SEQ ID NO 70
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 70

Ile Gly Pro Ala Gly Asp Thr
1 5

<210> SEQ ID NO 71
 <211> LENGTH: 51
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 71

gcaagcgagg ggatagcagt tcgtccggac gactactacg gtatggacgt c 51

<210> SEQ ID NO 72

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 72

Ala Ser Glu Gly Ile Ala Val Arg Pro Asp Asp Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> SEQ ID NO 73

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 73

gacatccagt tgaccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgct gggccagtca ggacattacc agttatttag cctggatca gaaaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg cagcttatta ctgtcaacag cttaatagtt acccgctcac tttcggcgga 300
gggaccaagg tggagatcaa acga 324

<210> SEQ ID NO 74

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 74

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Asp Ile Thr Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Lys Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ala Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg
100 105

<210> SEQ ID NO 75

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 75

caggacatta ccagttat

18

<210> SEQ ID NO 76
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 76

Gln Asp Ile Thr Ser Tyr
 1 5

<210> SEQ ID NO 77
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 77

gctgcatcc

9

<210> SEQ ID NO 78
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 78

Ala Ala Ser
 1

<210> SEQ ID NO 79
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 79

caacagctta atagttaccc gctcact

27

<210> SEQ ID NO 80
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 80

Gln Gln Leu Asn Ser Tyr Pro Leu Thr
 1 5

<210> SEQ ID NO 81
 <211> LENGTH: 381
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 81

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gaggtgcagc tgttgagtc tgggggagac ttggtacagc ctgggggggtc cctgagactc    60
tcctgtgcaa cctctggatt cagttttagt agtgatgcca tgaactgggt ccgccaggct    120
ccaggggaagg gcctggagtg ggtctcaggt attagtggta gtggtggtaa cacatactac    180
gcagactccg tgaagggccg gttcaccatc tccagagaca ttccaagag cacgctgtct    240
ctgcaaatga acagcctgag agccgaggac acggccgtat attattgtgc gaaagagggt    300
actaatatgg ttcggggagt tgttatggag gacaacggta tggacgtctg gggccaaggg    360
accacggtca ccgtctccgc c                                                    381

```

```

<210> SEQ ID NO 82
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 82

```

```

Glu Val Gln Leu Leu Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Gly
 1                5                10                15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Ser Phe Ser Ser Asp
                20                25                30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
                35                40                45
Ser Gly Ile Ser Gly Ser Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val
 50                55                60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Ile Ser Lys Ser Thr Leu Ser
65                70                75                80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                90                95
Ala Lys Glu Gly Thr Asn Met Val Arg Gly Val Val Met Glu Asp Asn
                100                105                110
Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ala
                115                120                125

```

```

<210> SEQ ID NO 83
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 83

```

```

ggattcagtt ttagtagtga tgcc                                                    24

```

```

<210> SEQ ID NO 84
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 84

```

```

Gly Phe Ser Phe Ser Ser Asp Ala
 1                5

```

```

<210> SEQ ID NO 85
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

```


-continued

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 85

attagtggta gtggtgtaa caca 24

<210> SEQ ID NO 86
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 86

Ile Ser Gly Ser Gly Gly Asn Thr
1 5

<210> SEQ ID NO 87
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 87

gcgaaagagg gtactaatat ggttcgggga gttgttatgg aggacaacgg tatggacgtc 60

<210> SEQ ID NO 88
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 88

Ala Lys Glu Gly Thr Asn Met Val Arg Gly Val Val Met Glu Asp Asn
1 5 10 15

Gly Met Asp Val
20

<210> SEQ ID NO 89
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 89

gacatccaga tgaccagtc gccatcttcc gtgtctgcat ctgtgggaga cagagtcacc 60

atcacttgtc gggcgagtca gggatttagc gactacttag cctggtatca gcagaaacca 120

ggaaaagccc ctaaactcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatcc 180

aggttcagcg gccgtggctc tgggacagat ttcactctca ccatcagcac cctgcagcct 240

gaagattttg caacttacta ttgtcaacag gtaaacagtt tcccgtcac tttcggcgga 300

gggaccaagg tggagatcaa acga 324

<210> SEQ ID NO 90
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 90

-continued

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg
 100 105

<210> SEQ ID NO 91
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 91

cagggtatta gcgactac

18

<210> SEQ ID NO 92
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 92

Gln Gly Ile Ser Asp Tyr
 1 5

<210> SEQ ID NO 93
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 93

gctgcatcc

9

<210> SEQ ID NO 94
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 94

Ala Ala Ser
 1

<210> SEQ ID NO 95
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 95

caacaggcta acagtttccc gctcact

27

<210> SEQ ID NO 96

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 96

Gln Gln Ala Asn Ser Phe Pro Leu Thr

1 5

<210> SEQ ID NO 97

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 97

caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcaat aactatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggcgtg ggtggcagtt atgtggtata gtgaaagtca taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctggaaatga acagcctgag agtcgaggac acggctatat attactgtgc gagagatctc 300

ggtgaccccg atgcttttga tatctggggc caagggacaa tggtcaccgt ctcttca 357

<210> SEQ ID NO 98

<211> LENGTH: 119

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 98

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asn Tyr
20 25 30Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Ala Trp Val
35 40 45Ala Val Met Trp Tyr Ser Glu Ser His Lys Tyr Tyr Ala Asp Ser Val
50 55 60Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80Leu Glu Met Asn Ser Leu Arg Val Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95Ala Arg Asp Leu Gly Asp Pro Asp Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110Thr Met Val Thr Val Ser Ser
115

<210> SEQ ID NO 99

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 99

ggattcacct tcaataacta tggc

24

<210> SEQ ID NO 100
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 100

Gly Phe Thr Phe Asn Asn Tyr Gly
1 5

<210> SEQ ID NO 101
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 101

atgtggtata gtgaaagtca taaa

24

<210> SEQ ID NO 102
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 102

Met Trp Tyr Ser Glu Ser His Lys
1 5

<210> SEQ ID NO 103
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 103

gcgagagatc tcggtgacct cgatgctttt gatatc

36

<210> SEQ ID NO 104
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 104

Ala Arg Asp Leu Gly Asp Pro Asp Ala Phe Asp Ile
1 5 10

<210> SEQ ID NO 105
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 105

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gacatccagt tgaccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc    60
atcacttgct gggccagtca gggcattagc agttatntag cctggtatca gcaaaaacca    120
gggaaagccc ctaagctcct gatttatggt gcatccactt tgcaaagtgg ggtcccatca    180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct    240
gaagattttg caacttatta ctgtcaacag cttaatagtt accctctcac cttcggcgga    300
gggaccaagg tggagatcaa acga                                           324

```

```

<210> SEQ ID NO 106
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 106

```

```

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1             5             10             15
Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Ser Tyr
 20             25             30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35             40             45
Tyr Gly Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50             55             60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65             70             75             80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Leu
 85             90             95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100             105

```

```

<210> SEQ ID NO 107
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 107

```

```

cagggcatta gcagttat                                           18

```

```

<210> SEQ ID NO 108
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 108

```

```

Gln Gly Ile Ser Ser Tyr
 1             5

```

```

<210> SEQ ID NO 109
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 109

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-continued

ggtgcatcc

9

<210> SEQ ID NO 110
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 110

Gly Ala Ser
 1

<210> SEQ ID NO 111
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 111

caacagctta atagttacc tctcacc

27

<210> SEQ ID NO 112
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 112

Gln Gln Leu Asn Ser Tyr Pro Leu Thr
 1 5

<210> SEQ ID NO 113
 <211> LENGTH: 375
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 113

caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcaggt atgtcatatg atggaagtag taaatactat 180
 gaagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgaat 240
 ctgcaaatga acagcctgag agttgaggac acggctgtgt attactgtgc gaaagaaagg 300
 gactacgttg agtacgtaga ctectactac ggtatggagc tctggggcca agggaccacg 360
 gtcaccgtct ccgcc 375

<210> SEQ ID NO 114
 <211> LENGTH: 125
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 114

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

-continued

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Gly Met Ser Tyr Asp Gly Ser Ser Lys Tyr Tyr Glu Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Asn
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Arg Asp Tyr Val Glu Tyr Val Asp Ser Tyr Tyr Gly Met
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ala
 115 120 125

<210> SEQ ID NO 115
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 115

ggattcacct tcagtagcta tggc

24

<210> SEQ ID NO 116
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 116

Gly Phe Thr Phe Ser Ser Tyr Gly
 1 5

<210> SEQ ID NO 117
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 117

atgtcatatg atggaagtag taaa

24

<210> SEQ ID NO 118
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 118

Met Ser Tyr Asp Gly Ser Ser Lys
 1 5

<210> SEQ ID NO 119
 <211> LENGTH: 54
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 119

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 gcgaaagaaa gggactacgt tgagtacgta gactcctact acggtatgga cgtc 54

<210> SEQ ID NO 120
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 120

Ala Lys Glu Arg Asp Tyr Val Glu Tyr Val Asp Ser Tyr Tyr Gly Met
 1 5 10 15

Asp Val

<210> SEQ ID NO 121
 <211> LENGTH: 324
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 121

gccatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
 gggaaagccc ctaaggtcct aatctatgct gcatccagtt taaaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tggaacagtt ttcactctca ccatcagcag cctgcagcct 240
 gaagatdddg caacttatta ctgtctacaa gattacaatt acccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa acga 324

<210> SEQ ID NO 122
 <211> LENGTH: 108
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 122

Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
 20 25 30
 Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Val Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asn Tyr Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> SEQ ID NO 123
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 123

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cagggcatta gaaatgat

18

<210> SEQ ID NO 124
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 124

Gln Gly Ile Arg Asn Asp
 1 5

<210> SEQ ID NO 125
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 125

gctgcatcc

9

<210> SEQ ID NO 126
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 126

Ala Ala Ser
 1

<210> SEQ ID NO 127
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 127

ctacaagatt acaattacc gctcact

27

<210> SEQ ID NO 128
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 128

Leu Gln Asp Tyr Asn Tyr Pro Leu Thr
 1 5

<210> SEQ ID NO 129
 <211> LENGTH: 375
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 129

gaggtgcagc tgggtggagtc tgggggaggt gtggtacggc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatggca tgagctgggt ccgccaattt 120

-continued

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ccaggaagg ggctggagt ggtctctagt attgatgaa atggtggtaa cacagggtat 180
tcagactctg tgaagggccg attcaccatc tccagagaca acgcaaaaa ctccctgcat 240
ctgcaaatga acagtctgag agccgaggac acggccttgt atcactgtgc gagagatccc 300
gattatgatt cegtttgggg gaattategt ccctttgact actggggcca gggaaccctg 360
gtcaccgtct cctca 375

```

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<210> SEQ ID NO 130
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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```

<400> SEQUENCE: 130

```

```

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
 1             5             10             15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
          20             25             30
Gly Met Ser Trp Val Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp Val
          35             40             45
Ser Ser Ile Asp Gly Asn Gly Gly Asn Thr Gly Tyr Ser Asp Ser Val
          50             55             60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu His
          65             70             75             80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
          85             90             95
Ala Arg Asp Pro Asp Tyr Asp Ser Val Trp Gly Asn Tyr Arg Pro Phe
          100            105            110
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
          115            120            125

```

```

<210> SEQ ID NO 131
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 131

```

```

ggattcacct ttgatgatta tggc 24

```

```

<210> SEQ ID NO 132
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 132

```

```

Gly Phe Thr Phe Asp Asp Tyr Gly
 1             5

```

```

<210> SEQ ID NO 133
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 133

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-continued

attgatggaa atggtggtaa caca 24

<210> SEQ ID NO 134
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 134

Ile Asp Gly Asn Gly Gly Asn Thr
 1 5

<210> SEQ ID NO 135
 <211> LENGTH: 54
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 135

gcgagagatc ccgattatga ttccgtttgg gggaattatc gtcctttga ctac 54

<210> SEQ ID NO 136
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 136

Ala Arg Asp Pro Asp Tyr Asp Ser Val Trp Gly Asn Tyr Arg Pro Phe
 1 5 10 15

Asp Tyr

<210> SEQ ID NO 137
 <211> LENGTH: 342
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 137

gatattgtga tgactcagtc tccagactcc ctggctgtgt ctctgggcca gagggccacc 60
 atcaactgca agtccagcca gagtgtttta tccagctcca acgataacaa ctacttagct 120
 tggttccagc agaaaccagg acagcctcct aacctactca tttactgggc atccaccgg 180
 gattccgggg tccctgaccg attcagtgcc agcgggtctg ggacagattt caccctcgcc 240
 atcagcagcc tgcaggctga agatgtggca gtttattact gtcaccaata ttatagttct 300
 cctccgacgt tcggccaagg gaccaaggtg gagatcaaac ga 342

<210> SEQ ID NO 138
 <211> LENGTH: 114
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 138

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Ser Ser

-continued

 caccaatatt atagttctcc tccgacg

27

<210> SEQ ID NO 144
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

 <400> SEQUENCE: 144

His Gln Tyr Tyr Ser Ser Pro Pro Thr
 1 5

<210> SEQ ID NO 145
 <211> LENGTH: 372
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 145

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
 acctgcactg tctctggtgg ctccattaac agtgggtggt attactggag ctggatccgc 120
 cagcaccag ggaagggcct ggagtggatt ggtacatct cttacagtgg gaataccaac 180
 tacaaccgt cctcaagag tcgagttacc atatcagtag acacgtctaa gaaccagttc 240
 tcctgacac tgacctctgt gactgccgcg gacacggccg tgtattactg tgcgagagac 300
 agtgacgtgg atacaggtct ggttgatggt tttgatgtct ggggccaagg aacaatggtc 360
 accgtctctt ca 372

<210> SEQ ID NO 146
 <211> LENGTH: 124
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 146

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Asn Ser Gly
 20 25 30
 Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
 35 40 45
 Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser
 50 55 60
 Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
 65 70 75 80
 Ser Leu Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Ser Asp Val Asp Thr Gly Leu Val Asp Gly Phe Asp
 100 105 110
 Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 147
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

-continued

 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 147

ggtggctcca ttaacagtgg tggttattac

30

<210> SEQ ID NO 148

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 148

Gly	Gly	Ser	Ile	Asn	Ser	Gly	Gly	Tyr	Tyr
1				5					10

<210> SEQ ID NO 149

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 149

atctcttaca gtggaatac c

21

<210> SEQ ID NO 150

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 150

Ile	Ser	Tyr	Ser	Gly	Asn	Thr
1				5		

<210> SEQ ID NO 151

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 151

gcgagagaca gtgacgtgga tacaggtctg gttgatgggtt ttgatgtc

48

<210> SEQ ID NO 152

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 152

Ala	Arg	Asp	Ser	Asp	Val	Asp	Thr	Gly	Leu	Val	Asp	Gly	Phe	Asp	Val
1				5				10					15		

<210> SEQ ID NO 153

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 153

-continued

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gatattgtga tgaccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcgagtca ggggtgtagc agctggtagc cctggtagc gcagaaacca 120
gggaaagccc ccaagctcct gatttatact acatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaggattttg caacttacta ttgtcaacag tctaacagtt ttccattcac tttcggcct 300
gggaccaagg tggagatcaa a 321

```

```

<210> SEQ ID NO 154
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 154

```

```

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1             5             10             15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Val Ser Ser Trp
 20             25             30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35             40             45
Tyr Thr Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50             55             60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65             70             75             80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Ser Phe Pro Phe
 85             90             95
Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
 100            105

```

```

<210> SEQ ID NO 155
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 155

```

```

cagggtgtta gcagctgg 18

```

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<210> SEQ ID NO 156
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 156

```

```

Gln Gly Val Ser Ser Trp
 1             5

```

```

<210> SEQ ID NO 157
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 157

```

```

actacatcc

```

-continued

<210> SEQ ID NO 158
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 158

Thr Thr Ser
 1

<210> SEQ ID NO 159
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 159

caacagtcta acagttttcc attcact

27

<210> SEQ ID NO 160
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 160

Gln Gln Ser Asn Ser Phe Pro Phe Thr
 1 5

<210> SEQ ID NO 161
 <211> LENGTH: 372
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 161

gaggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggc cctaagactc 60
 tctgtgcag cctctggatt ctccgtcagt tactacgaca tgcactgggt cgcceaagtt 120
 acaggaaaag gtctggagtg ggtctcagct attggtcctg caggtgacac atattacca 180
 ggctccgtga agggccgatt caccatctcc agagaagatg ccacgaactc cttatatctt 240
 caaatacaca gcctgggagc cggggacacg gctgtgtatt actgtgcaag agaggggggt 300
 atagcagctc gtccggacga ctactacggt atggacgtct ggggccaagg gaccacggtc 360
 accgtctcct ca 372

<210> SEQ ID NO 162
 <211> LENGTH: 124
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 162

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Val Ser Tyr Tyr
 20 25 30

-continued

<210> SEQ ID NO 168
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 168

Ala Arg Glu Gly Ala Ile Ala Ala Arg Pro Asp Asp Tyr Tyr Gly Met
 1 5 10 15

Asp Val

<210> SEQ ID NO 169
 <211> LENGTH: 324
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 169

gacatccagt tgaccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgct gggccagtca ggacattagc agttatttag cctggtatca gcaaaaacca 120
 gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtcaacaa cttaatagtt acccgctcac ttteggcgga 300
 gggaccaagg tggagatcaa acga 324

<210> SEQ ID NO 170
 <211> LENGTH: 108
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 170

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Asp Ile Ser Ser Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> SEQ ID NO 171
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 171

-continued

caggacatta gcagttat

18

<210> SEQ ID NO 172
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 172

Gln Asp Ile Ser Ser Tyr
 1 5

<210> SEQ ID NO 173
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 173

gctgcatcc

9

<210> SEQ ID NO 174
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 174

Ala Ala Ser
 1

<210> SEQ ID NO 175
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 175

caacaactta atagttacc gctcact

27

<210> SEQ ID NO 176
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 176

Gln Gln Leu Asn Ser Tyr Pro Leu Thr
 1 5

<210> SEQ ID NO 177
 <211> LENGTH: 363
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 177

gaggtgcagc tgggtggagtc tgggggagggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttggt gattatgcc tgcactgggt ccggcaagct 120

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ccaggaagg gcctggagt ggtctcaggt attaatttga atagtggcac cataggctat 180
gcgactctg tgaagggccg attcaccatt tcaagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccttct attactgtgc aaaagatata 300
gacggctact atcactacgc tatggacgtc tggggccaag ggaccacggt caccgtctcc 360
tca 363

```

```

<210> SEQ ID NO 178
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 178

```

```

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1             5             10             15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
 20             25             30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35             40             45
Ser Gly Ile Asn Leu Asn Ser Gly Thr Ile Gly Tyr Ala Asp Ser Val
 50             55             60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65             70             75             80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Phe Tyr Tyr Cys
 85             90             95
Ala Lys Asp Ile Asp Gly Tyr Tyr His Tyr Ala Met Asp Val Trp Gly
 100            105            110
Gln Gly Thr Thr Val Thr Val Ser Ser
 115            120

```

```

<210> SEQ ID NO 179
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 179

```

```

ggattcacct ttggtgatta tgcc 24

```

```

<210> SEQ ID NO 180
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 180

```

```

Gly Phe Thr Phe Gly Asp Tyr Ala
 1             5

```

```

<210> SEQ ID NO 181
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

```

<400> SEQUENCE: 181

```

-continued

 attaatttga atagtggcac cata

24

<210> SEQ ID NO 182
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

 <400> SEQUENCE: 182

Ile Asn Leu Asn Ser Gly Thr Ile
 1 5

<210> SEQ ID NO 183
 <211> LENGTH: 42
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

 <400> SEQUENCE: 183

gcaaaagata tagacggcta ctatcactac gctatggacg tc

42

<210> SEQ ID NO 184
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

 <400> SEQUENCE: 184

Ala Lys Asp Ile Asp Gly Tyr Tyr His Tyr Ala Met Asp Val
 1 5 10

<210> SEQ ID NO 185
 <211> LENGTH: 324
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

 <400> SEQUENCE: 185

gacatccagt tgaccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgct gggccagtca gggcattagc agttatntag cctgggatca gcaaaaacca 120

gggaaagccc ctaaactcct gatctatgat gcatccactt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttactctca caatcagcaa cctgcagcct 240

gaagattttg caacttatta ctgtcaacag gttaatagtt accctctcac tttcggcgga 300

gggaccaagg tggaaatcaa acga 324

<210> SEQ ID NO 186
 <211> LENGTH: 108
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

 <400> SEQUENCE: 186

Asp Val Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Ser Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

-continued

<212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 192

Gln Gln Val Asn Ser Tyr Pro Leu Thr
 1 5

<210> SEQ ID NO 193
 <211> LENGTH: 354
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 193

caggtgcagc tgggtggagtc tgggggagggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag cgtctggatt caccttcatt aactatggca tacattgggt ccgccagggt 120
 ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa tgaatggtat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtgtat 240
 ctggaaatga ataaactgag agccgaggac acggctgtgt attactgtgc gagagaagaa 300
 gaggactacg gtatggacgt ctgggggtcaa gggaccacgg tcaccgtctc ctca 354

<210> SEQ ID NO 194
 <211> LENGTH: 118
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 194

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ile Asn Tyr
 20 25 30
 Gly Ile His Trp Val Arg Gln Gly Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Glu Trp Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Glu Met Asn Lys Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Glu Glu Asp Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
 100 105 110
 Thr Val Thr Val Ser Ser
 115

<210> SEQ ID NO 195
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 195

ggattcacct tcattaacta tggc

24

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<210> SEQ ID NO 196
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 196

Gly Phe Thr Phe Ile Asn Tyr Gly
 1 5

<210> SEQ ID NO 197
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 197

atatggtatg atggaagtaa tgaa 24

<210> SEQ ID NO 198
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 198

Ile Trp Tyr Asp Gly Ser Asn Glu
 1 5

<210> SEQ ID NO 199
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 199

gcgagagaag aagaggacta cggtatggac gtc 33

<210> SEQ ID NO 200
 <211> LENGTH: 11
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 200

Ala Arg Glu Glu Glu Asp Tyr Gly Met Asp Val
 1 5 10

<210> SEQ ID NO 201
 <211> LENGTH: 339
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 201

gacatccaga tgaccagtc tocagactcc ctggctgtgt ctctgggcga gagggccgcc 60

atcaactgca agtccagcca gagtgtttta tacatctcca acaataaaa ctacttagct 120

tggtagcagc agaaaccagg acagccgct aagctcctca tttactgggc atccaccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

-continued

atcagcagcc tgcaggctga agatgtggct attattact gtcaacaata ttatagttct 300
 cctccgacgt tcggccaagg gaccaaagtg gatatcaaa 339

<210> SEQ ID NO 202
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 202

Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Ala Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ile
 20 25 30
 Ser Asn Asn Asn Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Ile Tyr Tyr Cys Gln Gln
 85 90 95
 Tyr Tyr Ser Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp Ile
 100 105 110

Lys

<210> SEQ ID NO 203
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 203

cagagtgttt tatacatctc caacaataac aactac 36

<210> SEQ ID NO 204
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 204

Gln Ser Val Leu Tyr Ile Ser Asn Asn Asn Asn Tyr
 1 5 10

<210> SEQ ID NO 205
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 205

tgggcatcc 9

<210> SEQ ID NO 206
 <211> LENGTH: 3
 <212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 206

Trp Ala Ser
 1

<210> SEQ ID NO 207
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 207

caacaatatt atagttctcc tccgacg 27

<210> SEQ ID NO 208
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 208

Gln Gln Tyr Tyr Ser Ser Pro Pro Thr
 1 5

<210> SEQ ID NO 209
 <211> LENGTH: 357
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 209

caggtgcagc tgggtggagtc tgggggaggc ttggttaagc ctggagggtc cctgagactc 60
 tctgtgcag cctctggatt caccttcagt gacttcaaca tgggctggat ccgccaggct 120
 ccaggaagg ggctggagtg ggtttcacac attagtggta gtggtaatgt catttactac 180
 gcagactctg tgaagggccg attcgccatc tccagggaca acggcaagaa ctoactgtat 240
 ctgcaagtga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatata 300
 ggtgactccg atgcgtttga tatctggggc caagggacaa tggtcaccgt ctcttca 357

<210> SEQ ID NO 210
 <211> LENGTH: 119
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 210

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Phe
 20 25 30

Asn Met Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser His Ile Ser Gly Ser Gly Asn Val Ile Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Gly Lys Asn Ser Leu Tyr

-continued

65		70		75		80									
Leu	Gln	Val	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Asp	Ile	Gly	Asp	Ser	Asp	Ala	Phe	Asp	Ile	Trp	Gly	Gln	Gly
			100					105					110		
Thr	Met	Val	Thr	Val	Ser	Ser									
			115												

<210> SEQ ID NO 211
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 211

ggattcacct tcagtgactt caac

24

<210> SEQ ID NO 212
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 212

Gly Phe Thr Phe Ser Asp Phe Asn
 1 5

<210> SEQ ID NO 213
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 213

attagtggtgta gtaggtaatgt catt

24

<210> SEQ ID NO 214
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 214

Ile Ser Gly Ser Gly Asn Val Ile
 1 5

<210> SEQ ID NO 215
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 215

gcgagagata tcggtgactc cgatgcgttt gatatc

36

<210> SEQ ID NO 216
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

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 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 216

Ala Arg Asp Ile Gly Asp Ser Asp Ala Phe Asp Ile
 1 5 10

<210> SEQ ID NO 217

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 217

gacatccagt tgaccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgct gggccagtca ggacattagc agttatttag cctgggatca gcaaaaacca 120
 gggaaagccc ctaagctcct gatctatggt gcatccactt tggaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
 gaagatgttg caacttatta ctgtcaacag cttaataactt acccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa acga 324

<210> SEQ ID NO 218

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 218

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Asp Ile Ser Ser Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Gly Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Thr Tyr Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> SEQ ID NO 219

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 219

caggacatta gcagttat 18

<210> SEQ ID NO 220

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 220

Gln Asp Ile Ser Ser Tyr
 1 5

<210> SEQ ID NO 221

<211> LENGTH: 9

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 221

ggtgcatcc

9

<210> SEQ ID NO 222

<211> LENGTH: 3

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 222

Gly Ala Ser
 1

<210> SEQ ID NO 223

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 223

caacagctta atacttacc gctcact

27

<210> SEQ ID NO 224

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 224

Gln Gln Leu Asn Thr Tyr Pro Leu Thr
 1 5

<210> SEQ ID NO 225

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 225

gaggtgcagc tgggtggagtc tgggggaggc ttggtacatc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt tacctttgat gattatgcca tgcactgggt ccggcaatct 120

ccaggaagg gcctggagtg ggtctcaggt attagttgga atagtgttat caaacactct 180

acggactctg tgaggggccc attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgaa acctgaggac acggcctttt attactgtgc aaaggatgag 300

gatgactgga actaccttga ctactggggc cagggaaacc tggtcaccgt ctctca 357

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<210> SEQ ID NO 226
 <211> LENGTH: 119
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

 <400> SEQUENCE: 226

 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Val Ile Lys His Ser Thr Asp Ser Val
 50 55 60
 Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Phe Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Glu Asp Asp Trp Asn Tyr Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

 Thr Leu Val Thr Val Ser Ser
 115

<210> SEQ ID NO 227
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 227

ggatttacct ttgatgatta tgcc

24

<210> SEQ ID NO 228
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 228

Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> SEQ ID NO 229
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 229

attagttgga atagtgttat caaa

24

<210> SEQ ID NO 230
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 230

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Ile Ser Trp Asn Ser Val Ile Lys
1 5

<210> SEQ ID NO 231
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 231

gcaaaggatg aggatgactg gaactacctt gactac 36

<210> SEQ ID NO 232
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 232

Ala Lys Asp Glu Asp Asp Trp Asn Tyr Leu Asp Tyr
1 5 10

<210> SEQ ID NO 233
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 233

gacatccaga tgaccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca ggatattaac agctggtag cctggatca gcagaaacca 120
gggaaagccc ctaaactcct gatctatact tcatccaatt tgcaaagtgg ggtcccatca 180
agattcagcg gcagtgggtc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag tctgacagtt tcccattcac ttctggcct 300
gggaccaaag tggatatcaa acga 324

<210> SEQ ID NO 234
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 234

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asn Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ser Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Ser Phe Pro Phe
85 90 95

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Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
 100 105

<210> SEQ ID NO 235
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 235

caggatatta acagctgg

18

<210> SEQ ID NO 236
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 236

Gln Asp Ile Asn Ser Trp
 1 5

<210> SEQ ID NO 237
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 237

acttcatcc

9

<210> SEQ ID NO 238
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 238

Thr Ser Ser
 1

<210> SEQ ID NO 239
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 239

caacagtctg acagtttccc attcact

27

<210> SEQ ID NO 240
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 240

Gln Gln Ser Asp Ser Phe Pro Phe Thr
 1 5

-continued

<210> SEQ ID NO 241
 <211> LENGTH: 366
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 241

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caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc   60
tcctgtgcag cgtctggatt cacctttagt aactatggca tgcactgggt ccgccaggct   120
ccaggcaagg ggctggagtg ggtggcacgt atatggtatg atggaagtaa taagtactat   180
gcagactccg tgaagggccg attcaccatc tccagagaca gttccaagaa cacgctgtat   240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagagggg   300
gagcagaacc tggactatta ccctttagac gtctggggcc aagggaccac ggtcaccgtc   360
tcctca                                           366
  
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<210> SEQ ID NO 242
 <211> LENGTH: 122
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 242

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20           25           30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35           40           45
Ala Arg Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Ser Ser Lys Asn Thr Leu Tyr
 65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85           90           95
Ala Arg Glu Gly Glu Gln Asn Leu Asp Tyr Tyr Pro Leu Asp Val Trp
 100          105          110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115          120
  
```

<210> SEQ ID NO 243
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 243

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ggattcacct ttagtaacta tggc                                           24
  
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<210> SEQ ID NO 244
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 244

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Gly Phe Thr Phe Ser Asn Tyr Gly
 1 5

<210> SEQ ID NO 245
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 245

atatggtatg atggaagtaa taag 24

<210> SEQ ID NO 246
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 246

Ile Trp Tyr Asp Gly Ser Asn Lys
 1 5

<210> SEQ ID NO 247
 <211> LENGTH: 45
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 247

gcgagagagg gggagcagaa cctggactat taccctttag acgtc 45

<210> SEQ ID NO 248
 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 248

Ala Arg Glu Gly Glu Gln Asn Leu Asp Tyr Tyr Pro Leu Asp Val
 1 5 10 15

<210> SEQ ID NO 249
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 249

gacatcgtga tgaccagtc tccatcctcc ctgtctgcat ctggttgaga cagagtcacc 60

atcacttgcc gggcaagtca ggacattaga aatgatttag gctggtatca acagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt taaaaactgg ggtcccatca 180

aggttcagcg gcagtgtatc tggcacagat ttcactctca ccatcagcag cctgcagcct 240

gaagatthttg caacttatta ctgtctacaa gattacactt accctctcac ttctggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 250
 <211> LENGTH: 107
 <212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 250

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp
 20 25 30
 Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Val Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Thr Tyr Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 251
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 251

caggacatta gaaatgat

18

<210> SEQ ID NO 252
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 252

Gln Asp Ile Arg Asn Asp
 1 5

<210> SEQ ID NO 253
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 253

gctgcatcc

9

<210> SEQ ID NO 254
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 254

Ala Ala Ser
 1

<210> SEQ ID NO 255

-continued

<211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 255

ctacaagatt acacttaccc tctcact

27

<210> SEQ ID NO 256
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 256

Leu Gln Asp Tyr Thr Tyr Pro Leu Thr
 1 5

<210> SEQ ID NO 257
 <211> LENGTH: 354
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 257

caggtgcagc tgggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tcctgcaagg cttctgggta cacctttacc agatatggta tcagctgggt gcgacaggcc 120
 cctggactag ggcttgagt gatgggctgg atcagcgctt acgatggata cacaaacttt 180
 gcacagaagt tccagggcag attcaccatg accacagaca catccacgaa cacagcctac 240
 atggaactga ggggcctgag atctgacgac acggccgtgt attactgtgc gagagaggag 300
 gaggatgctg cttttgatat ctggggccaa gggacaatgg tcaccgtctc ttca 354

<210> SEQ ID NO 258
 <211> LENGTH: 118
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 258

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30
 Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Ser Ala Tyr Asp Gly Tyr Thr Asn Phe Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Phe Thr Met Thr Thr Asp Thr Ser Thr Asn Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Arg Gly Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Glu Glu Asp Ala Ala Phe Asp Ile Trp Gly Gln Gly Thr
 100 105 110
 Met Val Thr Val Ser Ser
 115

-continued

<210> SEQ ID NO 259
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 259

ggttacacct ttaccagata tgggt

24

<210> SEQ ID NO 260
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 260

Gly Tyr Thr Phe Thr Arg Tyr Gly
 1 5

<210> SEQ ID NO 261
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 261

atcagcgctt acgatggata caca

24

<210> SEQ ID NO 262
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 262

Ile Ser Ala Tyr Asp Gly Tyr Thr
 1 5

<210> SEQ ID NO 263
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 263

gcgagagagg aggaggatgc tgcttttgat atc

33

<210> SEQ ID NO 264
 <211> LENGTH: 11
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 264

Ala Arg Glu Glu Glu Asp Ala Ala Phe Asp Ile
 1 5 10

<210> SEQ ID NO 265
 <211> LENGTH: 342
 <212> TYPE: DNA

-continued

<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 265

```

gacatcgtga tgaccagtc tccagactcc ctatgatgtgc ctctgggcca gagggccacc    60
atcaactgca agtccagcca gagtatttta ttcggctcca acaataaaaa ctacttagct    120
tggtaccagc agaaatcagg acagcctcca aagctgctca tttactgggc atctaccggg    180
gaatccgggg tcctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc    240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact    300
cctcacactt ttggccaggg gaccaagctg gagatcaaac ga                          342
  
```

<210> SEQ ID NO 266
 <211> LENGTH: 114
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 266

```

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Asp Val Pro Leu Gly
 1           5           10          15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Ile Leu Phe Gly
          20           25           30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Ser Gly Gln
          35           40           45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
          50           55           60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65           70           75           80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
          85           90           95
Tyr Tyr Ser Thr Pro His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
          100          105          110

Lys Arg
  
```

<210> SEQ ID NO 267
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 267

```

cagagtattt tattcggtc caacaataaa aactac                                36
  
```

<210> SEQ ID NO 268
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 268

```

Gln Ser Ile Leu Phe Gly Ser Asn Asn Lys Asn Tyr
 1           5           10
  
```

<210> SEQ ID NO 269
 <211> LENGTH: 9

-continued

<212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 269

tgggcatct

9

<210> SEQ ID NO 270
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 270

Trp Ala Ser
 1

<210> SEQ ID NO 271
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 271

cagcaatatt atagtactcc tcacact

27

<210> SEQ ID NO 272
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 272

Gln Gln Tyr Tyr Ser Thr Pro His Thr
 1 5

<210> SEQ ID NO 273
 <211> LENGTH: 372
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 273

cagggtgcagc tgcaggagtc gggcccagga ctgattaacc cttcacagac cctgtccgtc 60

acctgcactg tctctggtgg ctccatcagc agtgggtggtt attattggac ctggatacgc 120

cagcaccag gaaagggcct ggagtggatt ggtacatct cttacagtgg gaacaccaac 180

tataatccgt ccctcaagag tcgagttacc atatcagtag acacggctaa gaaccagttc 240

tcctgaagc tgagctctgt gactgccgcg gacacggccg tctacttctg tgcgagagac 300

agtgcagtgg acacagctat ggttgatggt attgatatct ggggccaagg gacaatggtc 360

accgtctctt ca 372

<210> SEQ ID NO 274
 <211> LENGTH: 124
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 274

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Ile Asn Pro Ser Gln
 1 5 10 15
 Thr Leu Ser Val Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
 20 25 30
 Gly Tyr Tyr Trp Thr Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
 35 40 45
 Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser
 50 55 60
 Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ala Lys Asn Gln Phe
 65 70 75 80
 Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe
 85 90 95
 Cys Ala Arg Asp Ser Asp Val Asp Thr Ala Met Val Asp Gly Ile Asp
 100 105 110
 Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 275

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 275

ggtggctcca tcagcagtg tggttattat

30

<210> SEQ ID NO 276

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 276

Gly Gly Ser Ile Ser Ser Gly Gly Tyr Tyr
 1 5 10

<210> SEQ ID NO 277

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 277

atctcttaca gtgggaacac c

21

<210> SEQ ID NO 278

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 278

Ile Ser Tyr Ser Gly Asn Thr
 1 5

<210> SEQ ID NO 279

<211> LENGTH: 48

-continued

<212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 279

gcgagagaca gtgacgtgga cacagctatg gttgatggta ttgatatc 48

<210> SEQ ID NO 280
 <211> LENGTH: 16
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 280

Ala Arg Asp Ser Asp Val Asp Thr Ala Met Val Asp Gly Ile Asp Ile
 1 5 10 15

<210> SEQ ID NO 281
 <211> LENGTH: 324
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 281

gacatccaga tgaccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgtc gggcgagtca ggatattagc agctggtag cctgggatca gcagaaaccg 120
 gggagagccc ctaaactcct gatctatact gcatccagtt taaaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
 gaagattttg caacttactt ttgtcaacag gctaacagtt tcccattcac ttcgggcct 300
 gggaccaaag tggatatcaa acga 324

<210> SEQ ID NO 282
 <211> LENGTH: 108
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 282

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Trp
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ala Asn Ser Phe Pro Phe
 85 90 95
 Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
 100 105

<210> SEQ ID NO 283
 <211> LENGTH: 18
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 283

caggatatta gcagctgg

18

<210> SEQ ID NO 284
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 284

Gln Asp Ile Ser Ser Trp
 1 5

<210> SEQ ID NO 285
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 285

actgcatcc

9

<210> SEQ ID NO 286
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 286

Thr Ala Ser
 1

<210> SEQ ID NO 287
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 287

caacaggcta acagtttccc attcact

27

<210> SEQ ID NO 288
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 288

Gln Gln Ala Asn Ser Phe Pro Phe Thr
 1 5

<210> SEQ ID NO 289
 <211> LENGTH: 369
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 289

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc cggggggggtc cctgagactc      60
tcctgtgtag cctctggatt caccttcagc agttttgccca tgagttgggt ccgccaggct      120
ccaggggaagg ggctggagtg ggtctcagtc attagtggta gtggtggcag cacaaatcac      180
gcagactccg tgaggggccc gttcaccatc tccagagaca attccctgaa cacggtgtat      240
ctacaaatgc acagtctgag agccgaggat acggccttat attactgtgt gaaagcggag      300
accagctctt cctactteta ctacggtatg gacgtctggg gcccaaggac cacggtcacc      360
gtctcctca                                                                    369

```

<210> SEQ ID NO 290

<211> LENGTH: 123

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 290

```

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10          15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Phe
          20          25          30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45
Ser Val Ile Ser Gly Ser Gly Gly Ser Thr Asn His Ala Asp Ser Val
          50          55          60
Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Leu Asn Thr Val Tyr
          65          70          75          80
Leu Gln Met His Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
          85          90          95
Val Lys Ala Glu Thr Ser Ser Ser Tyr Phe Tyr Tyr Gly Met Asp Val
          100         105         110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
          115         120

```

<210> SEQ ID NO 291

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 291

```

ggattcacct tcagcagttt tgcc                                                                    24

```

<210> SEQ ID NO 292

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 292

```

Gly Phe Thr Phe Ser Ser Phe Ala
 1           5

```

<210> SEQ ID NO 293

<211> LENGTH: 24

<212> TYPE: DNA

-continued

<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 293

attagtggtgta gtggtggcag caca 24

<210> SEQ ID NO 294
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 294

Ile Ser Gly Ser Gly Gly Ser Thr
 1 5

<210> SEQ ID NO 295
 <211> LENGTH: 48
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 295

gtgaaagcgg agaccagctc ttctacttc tactacggta tggacgctc 48

<210> SEQ ID NO 296
 <211> LENGTH: 16
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 296

Val Lys Ala Glu Thr Ser Ser Ser Tyr Phe Tyr Tyr Gly Met Asp Val
 1 5 10 15

<210> SEQ ID NO 297
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 297

gacatccagt tgaccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgct gggccagtca ggacattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagtcc ctaacctcct gatctatggt gcatcctctt tgcaacctgg ggtcccatca 180

cggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag ttaaataatt accccacttt cggcggaggg 300

accaagctgg agatcaaacy a 321

<210> SEQ ID NO 298
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 298

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly

-continued

1	5	10	15
Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Asp Ile Ser Ser Tyr	20	25	30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Asn Leu Leu Ile	35	40	45
Tyr Gly Ala Ser Ser Leu Gln Pro Gly Val Pro Ser Arg Phe Ser Gly	50	55	60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro	65	70	75
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Asn Tyr Pro Thr	85	90	95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg	100	105	

<210> SEQ ID NO 299
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 299

caggacatta gcagttat

18

<210> SEQ ID NO 300
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 300

Gln Asp Ile Ser Ser Tyr
 1 5

<210> SEQ ID NO 301
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 301

ggtgcatcc

9

<210> SEQ ID NO 302
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 302

Gly Ala Ser
 1

<210> SEQ ID NO 303
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 303

-continued

caacagttaa ataattaccc cact

24

<210> SEQ ID NO 304
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 304

Gln Gln Leu Asn Asn Tyr Pro Thr
 1 5

<210> SEQ ID NO 305
 <211> LENGTH: 363
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 305

gaagtgcagc tgggtggagtc tgggggaggt gtggtacggc ctgggggggtc cctgagactc 60
 tctctgtcag cctctggatt cacctttgat gattatgccca tgcactgggt ccggcaagct 120
 ccaggggaagg gcctggagtg ggtcgcaggc attagttgga atagtggtag tatagactat 180
 gcggactctg tgaagggccg attcaccatt tccagagaca acgccccaaa ctccctgtat 240
 ctgcaaatga acagtctgcg agctggggac acggccttgt attactgtgc aaaagatatt 300
 ctggatctag actactacgg tttggacgtc tggggccaag ggaccacggt caccgtctcc 360
 tca 363

<210> SEQ ID NO 306
 <211> LENGTH: 121
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 306

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Asp Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Ile Leu Asp Leu Asp Tyr Tyr Gly Leu Asp Val Trp Gly
 100 105 110
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 307
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 307

ggattcacct ttgatgatta tgcc

24

<210> SEQ ID NO 308
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 308

Gly Phe Thr Phe Asp Asp Tyr Ala
 1 5

<210> SEQ ID NO 309
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 309

attagttgga atagtggtag tata

24

<210> SEQ ID NO 310
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 310

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> SEQ ID NO 311
 <211> LENGTH: 42
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 311

gcaaaagata ttctggatct agactactac ggtttgacg tc

42

<210> SEQ ID NO 312
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 312

Ala Lys Asp Ile Leu Asp Leu Asp Tyr Tyr Gly Leu Asp Val
 1 5 10

<210> SEQ ID NO 313
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 313

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gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc    60
atcacttgcc gggcgagtca ggacattagc agttatntag cctggtatca gcagaaacca    120
gggaaagttc ctaacctcct gatctatgat gcacaccttt tgcaatcagg ggtcccatct    180
cggttcagtg gcagtggatc tgggacagat ttcactctca ccctcagcag cctgcagcct    240
gaagattttg ctagttatta ctgtcaaaat tataacagtg ccccgtagac ttttggccag    300
gggaccaagc tggagatcaa a                                             321

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<210> SEQ ID NO 314
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 314

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1             5             10             15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr
 20             25             30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Asn Leu Leu Ile
 35             40             45
Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50             55             60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Leu Ser Ser Leu Gln Pro
 65             70             75             80
Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Asn Tyr Asn Ser Ala Pro Tyr
 85             90             95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100             105

```

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<210> SEQ ID NO 315
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 315

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caggacatta gcagttat                                             18

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<210> SEQ ID NO 316
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 316

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```

Gln Asp Ile Ser Ser Tyr
 1             5

```

```

<210> SEQ ID NO 317
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 317

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gatgcatcc

9

<210> SEQ ID NO 318
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 318

Asp Ala Ser
 1

<210> SEQ ID NO 319
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 319

caaaaattata acagtgtccc gtacact

27

<210> SEQ ID NO 320
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 320

Gln Asn Tyr Asn Ser Ala Pro Tyr Thr
 1 5

<210> SEQ ID NO 321
 <211> LENGTH: 366
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 321

gaagtgaac tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
 ccaggaagg gcctggagtg ggtctcaagt attagttgga atagtggtag cataggctat 180
 gcggactctg tgaagggccg attcaccatt tccagagaca acgccaagaa ttccctgtat 240
 cttcaaatga acagtctgaa acctgaggac acggccttgt attactgtac aaaagatacc 300
 gactacggtg actaccttga tgcttttgat atctggggcc aagggacaat ggtegcgcgc 360
 gcttca 366

<210> SEQ ID NO 322
 <211> LENGTH: 122
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 322

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

-continued

 acaaaagata ccgactacgg tgactacctt gatgcttttg atatc

45

<210> SEQ ID NO 328
 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 328

Thr Lys Asp Thr Asp Tyr Gly Asp Tyr Leu Asp Ala Phe Asp Ile
 1 5 10 15

<210> SEQ ID NO 329
 <211> LENGTH: 339
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 329

gatattgtga tgaccagtc tccagactcc ctggctgtgt ctctgggcca gagggccacc 60
 atcaactgca agtccagcca gagggtttta tacaactccg acaataagaa gtacttagct 120
 tgggtaccagc agaaacctgg acagcctcct aagctgctca tttactgggc atctaccggg 180
 gaatccgggg tcctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
 atcagcagcc tgcaggctga ggatgtggca gtttattact gtcaccaata ttatactact 300
 cctccgacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> SEQ ID NO 330
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 330

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Asn
 20 25 30
 Ser Asp Asn Lys Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His Gln
 85 90 95
 Tyr Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110

Lys

<210> SEQ ID NO 331
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 331

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cagagtgttt tatacaactc cgacaataag aagtac

36

<210> SEQ ID NO 332
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 332

Gln Ser Val Leu Tyr Asn Ser Asp Asn Lys Lys Tyr
 1 5 10

<210> SEQ ID NO 333
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 333

tgggcatct

9

<210> SEQ ID NO 334
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 334

Trp Ala Ser
 1

<210> SEQ ID NO 335
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 335

caccaatatt atactactcc tccgacg

27

<210> SEQ ID NO 336
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 336

His Gln Tyr Tyr Thr Thr Pro Pro Thr
 1 5

<210> SEQ ID NO 337
 <211> LENGTH: 357
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 337

gaggtgcagc tgggtggagtc tgggggaggt gtggtacggc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatggca tgagctgggt ccgccaagct 120

-continued

ccaggggaagg ggctggagtg tgtctctggt attaattgga atggtggtag cacagattat 180
gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agccgaggac acggcctcgt attactgtgc gagagatggt 300
ggggattggg actacttcga tctctggggc cgtggcaccc tggtcactgt ctctca 357

<210> SEQ ID NO 338
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 338

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Cys Val
35 40 45
Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Asp Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ser Tyr Tyr Cys
85 90 95
Ala Arg Asp Gly Gly Asp Trp Asp Tyr Phe Asp Leu Trp Gly Arg Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 339
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 339

ggattcacct ttgatgatta tggc 24

<210> SEQ ID NO 340
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 340

Gly Phe Thr Phe Asp Asp Tyr Gly
1 5

<210> SEQ ID NO 341
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 341

attaattgga atggtggtag caca 24

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<210> SEQ ID NO 342
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 342

Ile Asn Trp Asn Gly Gly Ser Thr
 1 5

<210> SEQ ID NO 343
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 343

gcgagagatg gtggggattg ggactacttc gatctc 36

<210> SEQ ID NO 344
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 344

Ala Arg Asp Gly Gly Asp Trp Asp Tyr Phe Asp Leu
 1 5 10

<210> SEQ ID NO 345
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 345

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60
 ctctcctgca gggccagtca gagtgtagc agcaacttag cctggtacca gcagaaacct 120
 ggccaggctc ccaggctcct catatatgga gcatccacca gggccactgg tatcccagcc 180
 aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
 gaagatattg cagtttattt ctgtcaggag tataatgact ggccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 346
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 346

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

-continued

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Glu Tyr Asn Asp Trp Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 347
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 347

cagagtgtta gcagcaac

18

<210> SEQ ID NO 348
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 348

Gln Ser Val Ser Ser Asn
 1 5

<210> SEQ ID NO 349
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 349

ggagcatcc

9

<210> SEQ ID NO 350
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 350

Gly Ala Ser
 1

<210> SEQ ID NO 351
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 351

caggagtata atgactggcc gctcact

27

<210> SEQ ID NO 352
 <211> LENGTH: 9
 <212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 352

Gln Glu Tyr Asn Asp Trp Pro Leu Thr
 1 5

<210> SEQ ID NO 353
 <211> LENGTH: 357
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 353

gaggtgcaac tgggtggagtc tgggggaggt gtggtacggc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatggca tgagctgggt ccgccaagct 120
 ccaggaagg ggctggagtg tgtctctggt attagttgga atggtggtaa cacagattat 180
 gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agccgaggac acggccttgt atcactgtgc gagagatggt 300
 ggggattggg actacttcca tctctggggc cgtggcaccc tggtcactgt ctctca 357

<210> SEQ ID NO 354
 <211> LENGTH: 119
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 354

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Cys Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Gly Gly Asn Thr Asp Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
 85 90 95
 Ala Arg Asp Gly Gly Asp Trp Asp Tyr Phe Asp Leu Trp Gly Arg Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> SEQ ID NO 355
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 355

ggattcacct ttgatgatta tggc 24

<210> SEQ ID NO 356

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<211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 356

Gly Phe Thr Phe Asp Asp Tyr Gly
 1 5

<210> SEQ ID NO 357
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 357

attagttgga atggtggtaa caca 24

<210> SEQ ID NO 358
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 358

Ile Ser Trp Asn Gly Gly Asn Thr
 1 5

<210> SEQ ID NO 359
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 359

gcgagagatg gtggggattg ggactacttc gatctc 36

<210> SEQ ID NO 360
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 360

Ala Arg Asp Gly Gly Asp Trp Asp Tyr Phe Asp Leu
 1 5 10

<210> SEQ ID NO 361
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 361

gaaatactga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagggttagt agcaacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catatatgga gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtggtc tgggacagag ttcactotta ccatcagcag cctgcagtct 240

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gaagattttg caatttatta ctgtcaggag tataatgact ggccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 362
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 362

Glu Ile Leu Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80
 Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Glu Tyr Asn Asp Trp Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 363
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 363

cagagtgtta gtagcaac 18

<210> SEQ ID NO 364
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 364

Gln Ser Val Ser Ser Asn
 1 5

<210> SEQ ID NO 365
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 365

ggagcatcc 9

<210> SEQ ID NO 366
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 366

Gly Ala Ser
1<210> SEQ ID NO 367
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 367

caggagtata atgactggcc gctcact 27

<210> SEQ ID NO 368
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 368

Gln Glu Tyr Asn Asp Trp Pro Leu Thr
1 5<210> SEQ ID NO 369
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 369

gaagtgaac tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatgcca tgtactgggt ccggcaagct 120
ccaggaagg gcctggagtg ggtctcaggt attagttgga atagtggcag cataggctat 180
gcgactctg tgaagggccg attcaccatc tctagagaca acgccaagaa ctccctgtat 240
ctgcaaattg acagcctgag agctgaggac acggccttgt attactgtgc aagagatatg 300
atggaagttg acctctacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 360
tca 363<210> SEQ ID NO 370
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 370

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30
Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

-continued

Leu Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Arg Asp Met Met Glu Val Asp Leu Tyr Gly Met Asp Val Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 371
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 371

ggattcacct ttgatgatta tgcc

24

<210> SEQ ID NO 372
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 372

Gly Phe Thr Phe Asp Asp Tyr Ala
 1 5

<210> SEQ ID NO 373
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 373

attagttgga atagtggcag cata

24

<210> SEQ ID NO 374
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 374

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> SEQ ID NO 375
 <211> LENGTH: 42
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 375

gcaagagata tgatggaagt tgacctctac ggtatggacg tc

42

<210> SEQ ID NO 376
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 376

Ala Arg Asp Met Met Glu Val Asp Leu Tyr Gly Met Asp Val
 1 5 10

<210> SEQ ID NO 377

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 377

gacatccaga tgaccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacg 60
 atcacttgtc gggcgagtca ggatattagc agttggttag cctgggatca gcagaaacca 120
 gggacagccc ctaagttcct gatctatgaa acatccagtt tgcaaagtgg ggteccctca 180
 aggttcagcg gcagtggatc tgggacagat ttcattctca ccatcagtag cctgcagcct 240
 gaagatthtg caacttacta ttgtcaacaa actgacagtt tcccgcacac ttttggccag 300
 gggaccaagc tggagatcag a 321

<210> SEQ ID NO 378

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 378

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Trp
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Phe Leu Ile
 35 40 45
 Tyr Glu Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Asp Ser Phe Pro His
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Arg
 100 105

<210> SEQ ID NO 379

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 379

caggatatta gcagttgg 18

<210> SEQ ID NO 380

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 380

Gln Asp Ile Ser Ser Trp
 1 5

<210> SEQ ID NO 381
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 381

gaaacatcc

9

<210> SEQ ID NO 382
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 382

Glu Thr Ser
 1

<210> SEQ ID NO 383
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 383

caacaaactg acagtttccc gcacact

27

<210> SEQ ID NO 384
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 384

Gln Gln Thr Asp Ser Phe Pro His Thr
 1 5

<210> SEQ ID NO 385
 <211> LENGTH: 357
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 385

gaggatgcagc tgggtggagtc tgggggaggt gtggtacggc ctggggggtc cctgagactc 60

tcctgtgtag cctctggatt cacctttgat gattatggca tgagctgggt ccgccaagct 120

ccaggaagg ggctggagt tgtctctggt attaattgga atggtggtag cacagattat 180

gcagactctg tgaagggccg attcactatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agccgaggac acggccttgt atcactgtgc gagagatggt 300

ggggattggg actacttcca tctctggggc cgtggcacc tggctactgt ctctca 357

<210> SEQ ID NO 386

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<211> LENGTH: 119
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

 <400> SEQUENCE: 386

 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Cys Val
 35 40 45
 Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Asp Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
 85 90 95
 Ala Arg Asp Gly Gly Asp Trp Asp Tyr Phe Asp Leu Trp Gly Arg Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> SEQ ID NO 387
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

 <400> SEQUENCE: 387

ggattcacct ttgatgatta tggc

24

<210> SEQ ID NO 388
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

 <400> SEQUENCE: 388

Gly Phe Thr Phe Asp Asp Tyr Gly
1 5

<210> SEQ ID NO 389
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

 <400> SEQUENCE: 389

attaattgga atggtgtag caca

24

<210> SEQ ID NO 390
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

 <400> SEQUENCE: 390

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Ile Asn Trp Asn Gly Gly Ser Thr
1 5

<210> SEQ ID NO 391
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 391

gcgagagatg gtggggattg ggactacttc gatctc 36

<210> SEQ ID NO 392
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 392

Ala Arg Asp Gly Gly Asp Trp Asp Tyr Phe Asp Leu
1 5 10

<210> SEQ ID NO 393
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 393

gaaatactga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60
ctctcctgca gggccagtc gagtgtagc agcaacttag cctggtacca gcagaaacct 120
ggccaggctc ccaggctcct catatatgga gcatccacca gggccactgg tatcccagcc 180
aggttcagtg gcagtggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
gaagattttg caattatta ctgtcaggag tataatgact ggccgctcac ttccggcgga 300
gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 394
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 394

Glu Ile Leu Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Glu Tyr Asn Asp Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

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100	105	
<210> SEQ ID NO 395		
<211> LENGTH: 18		
<212> TYPE: DNA		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic		
<400> SEQUENCE: 395		
cagagtgtta gcagcaac		18
<210> SEQ ID NO 396		
<211> LENGTH: 6		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic		
<400> SEQUENCE: 396		
Gln Ser Val Ser Ser Asn		
1 5		
<210> SEQ ID NO 397		
<211> LENGTH: 9		
<212> TYPE: DNA		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic		
<400> SEQUENCE: 397		
ggagcatcc		9
<210> SEQ ID NO 398		
<211> LENGTH: 3		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic		
<400> SEQUENCE: 398		
Gly Ala Ser		
1		
<210> SEQ ID NO 399		
<211> LENGTH: 27		
<212> TYPE: DNA		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic		
<400> SEQUENCE: 399		
caggagtata atgactggcc gctcact		27
<210> SEQ ID NO 400		
<211> LENGTH: 9		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic		
<400> SEQUENCE: 400		
Gln Glu Tyr Asn Asp Trp Pro Leu Thr		
1 5		
<210> SEQ ID NO 401		

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<211> LENGTH: 357
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 401

gaggtgcaac tgggtggagtc tgggggagggc ctggtcaagc ctgggggggtc cctgagactc 60
 tctctgttag cctctggatt caccttcagt agctataaca tgaactgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcattt ataagtggta gtagtaatta catacactac 180
 gcagactcag tgaagggccg attcaccatt tccagagaca acgccaagaa tgcactgtat 240
 ctgcagatga acagcctgag agccgaggac acggctgtat attactgtgc gagagacgac 300
 ggtgactacg actggttcga cccctggggc cagggaaacc tggtcacctg ctctca 357

<210> SEQ ID NO 402
 <211> LENGTH: 119
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 402

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Asn Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Phe Ile Ser Gly Ser Ser Asn Tyr Ile His Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ala Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Asp Gly Asp Tyr Asp Trp Phe Asp Pro Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> SEQ ID NO 403
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 403

ggattcacct tcagtagcta taac 24

<210> SEQ ID NO 404
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 404

Gly Phe Thr Phe Ser Ser Tyr Asn
 1 5

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<210> SEQ ID NO 405
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 405

ataagtggtgta gtagtaatta cata 24

<210> SEQ ID NO 406
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 406

Ile Ser Gly Ser Ser Asn Tyr Ile
 1 5

<210> SEQ ID NO 407
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 407

gcgagagacg acggtgacta cgactggttc gacccc 36

<210> SEQ ID NO 408
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 408

Ala Arg Asp Asp Gly Asp Tyr Asp Trp Phe Asp Pro
 1 5 10

<210> SEQ ID NO 409
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 409

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcctgca gggccagtca gagtgttagt agtagttact tagcctggta ccagcaaaaa 120
 cctggccagg ctcccaggct cctcatctat ggtacatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgta ttactgtcag cagtatgata actcatacac ttttggccag 300
 gggaccaagc tggagatcaa a 321

<210> SEQ ID NO 410
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 410

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gly Thr Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Asn Ser Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> SEQ ID NO 411

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 411

cagagtgtta gtagtagtta c

21

<210> SEQ ID NO 412

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 412

Gln Ser Val Ser Ser Ser Tyr
 1 5

<210> SEQ ID NO 413

<211> LENGTH: 9

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 413

ggtacatcc

9

<210> SEQ ID NO 414

<211> LENGTH: 3

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 414

Gly Thr Ser
 1

<210> SEQ ID NO 415

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 415

cagcagtatg ataactcata cact

24

<210> SEQ ID NO 416

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 416

Gln Gln Tyr Asp Asn Ser Tyr Thr
1 5

<210> SEQ ID NO 417

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 417

gaggtgcagc tgggtgcagtc tgggggaggc ctggtcaagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt aactttaaca tgaactgggt cgcgccaggct 120
 ccaggggaagg ggctggagtg ggtctcattc attagtagtc ttagtactta tacatactac 180
 gcagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcaactgtat 240
 ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagacgac 300
 ggtgaccacg actggttcga cccctggggc cagggaaacc tggtcacctg ctctca 357

<210> SEQ ID NO 418

<211> LENGTH: 119

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 418

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Phe
20 25 30
 Asn Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
 Ser Phe Ile Ser Ser Leu Ser Thr Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
 Ala Arg Asp Asp Gly Asp His Asp Trp Phe Asp Pro Trp Gly Gln Gly
100 105 110
 Thr Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 419

<211> LENGTH: 24

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<212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 419

ggattcacct tcagtaactt taac

24

<210> SEQ ID NO 420
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 420

Gly Phe Thr Phe Ser Asn Phe Asn
 1 5

<210> SEQ ID NO 421
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 421

attagtagtc ttagtactta taca

24

<210> SEQ ID NO 422
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 422

Ile Ser Ser Leu Ser Thr Tyr Thr
 1 5

<210> SEQ ID NO 423
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 423

gcgagagacg acggtgacca cgactgggttc gacccc

36

<210> SEQ ID NO 424
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 424

Ala Arg Asp Asp Gly Asp His Asp Trp Phe Asp Pro
 1 5 10

<210> SEQ ID NO 425
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 425

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gaaattgtgt tgacgcagtc tccagacacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtgtagt agcaactact tagcctggta ccaacaaaaa      120
cctggccagg ctcccaggct cctcatctat agtgcaccca acagggccac tggcatccca      180
gacagattca gtggcagtgg gtctgggaca gacttcactc tcaccatcag ccgactggag      240
cctgaagatt ttgcagtgta ttactgtcaa cagtatgata gttcatacac ttttggccag      300
gggaccaagc tggagatcaa a                                             321

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<210> SEQ ID NO 426

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 426

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Glu Ile Val Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly
 1             5             10             15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
          20             25             30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
          35             40             45
Ile Tyr Ser Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50             55             60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65             70             75             80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Ser Ser Tyr
          85             90             95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
          100             105

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<210> SEQ ID NO 427

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 427

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cagagtgtta gtagcaacta c                                             21

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<210> SEQ ID NO 428

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 428

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Gln Ser Val Ser Ser Asn Tyr
 1             5

```

<210> SEQ ID NO 429

<211> LENGTH: 9

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 429

agtgcaccc

9

<210> SEQ ID NO 430

<211> LENGTH: 3

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 430

Ser Ala Ser

1

<210> SEQ ID NO 431

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 431

caacagtatg atagttcata cact

24

<210> SEQ ID NO 432

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 432

Gln Gln Tyr Asp Ser Ser Tyr Thr

1

5

<210> SEQ ID NO 433

<211> LENGTH: 363

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 433

gaaatgcagc tggtagagtc tgggggaggc ttggtacagc ctgacaggtc cctgagactc 60

tcctgtgcag cctctggatt caactttgat aattatgcca tacactgggt ccggcaagct 120

ccagggaagg gcctcgagtg ggtctcaggt attagttgga atagtggtaa cataggttat 180

gcgactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgttt 240

ctgctaataga acagtctgag acctgacgac tcggccttgt attactgtac aagaggatac 300

aactggaacg cgttatccc tatggacgtc tggggccaag ggaccacggt caccgtctcc 360

tca

363

<210> SEQ ID NO 434

<211> LENGTH: 121

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 434

Glu Met Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Asp Arg

1

5

10

15

-continued

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe Asp Asn Tyr
 20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Asn Ile Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe
 65 70 75 80

Leu Leu Met Asn Ser Leu Arg Pro Asp Asp Ser Ala Leu Tyr Tyr Cys
 85 90 95

Thr Arg Gly Tyr Asn Trp Asn Ala Leu Ser Pro Met Asp Val Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 435
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 435

ggattcaact ttgataatta tgcc

24

<210> SEQ ID NO 436
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 436

Gly Phe Asn Phe Asp Asn Tyr Ala
 1 5

<210> SEQ ID NO 437
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 437

attagttgga atagtggtaa cata

24

<210> SEQ ID NO 438
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 438

Ile Ser Trp Asn Ser Gly Asn Ile
 1 5

<210> SEQ ID NO 439
 <211> LENGTH: 42
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 439

acaagaggat acaactggaa cgcggttatcc cctatggacg tc 42

<210> SEQ ID NO 440

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 440

Thr Arg Gly Tyr Asn Trp Asn Ala Leu Ser Pro Met Asp Val
 1 5 10

<210> SEQ ID NO 441

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 441

gacatccaaa tgaccagtc tccatcctcc ctgtctgcat ctgtagggga cagagtcacc 60
 gtcacttgcc gggcgagtca gggcattagc aattatntag cctggtatca gcaaaaacct 120
 ggtaaagttc ctaaactcct gatctatgct gcatccactt tgcaatcagg ggtcccatct 180
 cggttcagtg gcagtgatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
 gaagatggtg caagttatta ctgtcaaaac tataacagtg cccctatgac gttcggccaa 300
 gggaccaagg tggaaatcaa a 321

<210> SEQ ID NO 442

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 442

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Val Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Val Ala Ser Tyr Tyr Cys Gln Asn Tyr Asn Ser Ala Pro Met
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 443

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 443

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cagggcatta gcaattat

18

<210> SEQ ID NO 444
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 444

Gln Gly Ile Ser Asn Tyr
 1 5

<210> SEQ ID NO 445
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 445

gctgcatcc

9

<210> SEQ ID NO 446
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 446

Ala Ala Ser
 1

<210> SEQ ID NO 447
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 447

caaaactata acagtcccc tatgacg

27

<210> SEQ ID NO 448
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 448

Gln Asn Tyr Asn Ser Ala Pro Met Thr
 1 5

<210> SEQ ID NO 449
 <211> LENGTH: 366
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 449

caggtgcagc tacaacagtg ggacgcagga ctgttgaagc cttcggagac cctgtccctc 60

acctgcgctg tctatggtgg gtccttcagt tcttactact ggagctggat ccgccagccc 120

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ccaggggaagg ggctggaatg gattggggaa atcaatcatc gtggaagcac caactacaac 180
ccgtccctca agagtcgagt caccatctca gtagacacgt ccaagaacca gttctcccta 240
aagctgaggt ctgtgaccgc cgccgacacg gctgtgtatt actgtgacgc agggggggta 300
gcagctcgtc cggactggca cttctttgac tactggggcc agggaaccct ggtcaccgtc 360
tcctca 366

```

```

<210> SEQ ID NO 450
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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```

<400> SEQUENCE: 450

```

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Gln Val Gln Leu Gln Gln Trp Asp Ala Gly Leu Leu Lys Pro Ser Glu
 1             5             10             15
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Ser Tyr
          20             25             30
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
          35             40             45
Gly Glu Ile Asn His Arg Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
          50             55             60
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
          65             70             75             80
Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
          85             90             95
Arg Gly Gly Val Ala Ala Arg Pro Asp Trp His Phe Phe Asp Tyr Trp
          100            105            110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
          115            120

```

```

<210> SEQ ID NO 451
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 451

```

```

ggtgggtcct tcagttctta ctac 24

```

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<210> SEQ ID NO 452
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 452

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Gly Gly Ser Phe Ser Ser Tyr Tyr
 1             5

```

```

<210> SEQ ID NO 453
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 453

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-continued

atcaatcatc gtggaagcac c

21

<210> SEQ ID NO 454
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 454

Ile Asn His Arg Gly Ser Thr
 1 5

<210> SEQ ID NO 455
 <211> LENGTH: 48
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 455

gcgcgagggg gggtagcagc tcgtccggac tggcacttct ttgactac

48

<210> SEQ ID NO 456
 <211> LENGTH: 16
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 456

Ala Arg Gly Gly Val Ala Ala Arg Pro Asp Trp His Phe Phe Asp Tyr
 1 5 10 15

<210> SEQ ID NO 457
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 457

gacatccaga tgaccagtc tccatcctcc ctctctgcct ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca ggtcattcga aatgatttag gctggtttca gcagagacca 120

gggaaagccc ctaagcgct gatctatgct gcatccagtt taaaaagtga ggtcccatca 180

agattcagcg gcagtggatc tgggacagaa ttcactctca caatcaccag cctgcagcct 240

gaagatthtg caacttatta ctgtcttcag cataatagtt acccgctcac ctccggccaa 300

gggacacgac tggagattaa a 321

<210> SEQ ID NO 458
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 458

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Val Ile Arg Asn Asp
 20 25 30

-continued

<211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 464

Leu Gln His Asn Ser Tyr Pro Leu Thr
 1 5

<210> SEQ ID NO 465
 <211> LENGTH: 357
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 465

gagggtgcagc tgggtggagtc tgggggaggt gtggtacggc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatggca tgagctgggt ccgccaagtt 120
 ccaggggaagg ggctggagtg ggtctctggt cttaattgga atggtggaat cacaggttat 180
 acagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agccgaggac acggccttct atcactgtgc gcgagatagt 300
 ggggatcagg atgcttttga tatatggggc caggggacaa tggtcaccgt ctctca 357

<210> SEQ ID NO 466
 <211> LENGTH: 119
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 466

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Gly Met Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Leu Asn Trp Asn Gly Gly Ile Thr Gly Tyr Thr Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Phe Tyr His Cys
 85 90 95
 Ala Arg Asp Ser Gly Asp Gln Asp Ala Phe Asp Ile Trp Gly Gln Gly
 100 105 110
 Thr Met Val Thr Val Ser Ser
 115

<210> SEQ ID NO 467
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 467

ggattcacct ttgatgatta tggc

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<210> SEQ ID NO 468
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 468

Gly Phe Thr Phe Asp Asp Tyr Gly
 1 5

<210> SEQ ID NO 469
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 469

cttaattgga atggtggaat caca

24

<210> SEQ ID NO 470
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 470

Leu Asn Trp Asn Gly Gly Ile Thr
 1 5

<210> SEQ ID NO 471
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 471

gcgagagata gtgggatca ggatgctttt gatata

36

<210> SEQ ID NO 472
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 472

Ala Arg Asp Ser Gly Asp Gln Asp Ala Phe Asp Ile
 1 5 10

<210> SEQ ID NO 473
 <211> LENGTH: 318
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 473

caaatagtga tgacgcagtc tccagccacc ctgtctgtat ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtattact ccctacttag cctggtacca gcaaaaacct 120

ggccagactc ccaggctcct catctatggt gtatccacc gggccactgg tatccagcc 180

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aggttcagtgcgcagtggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttatta ctgtcagcag tatgacaact ggtatacttt tggccagggg 300
accaagctgg agatcaaa 318

```

```

<210> SEQ ID NO 474
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 474

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```

Gln Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
 1             5             10             15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Thr Pro Tyr
          20             25             30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Thr Pro Arg Leu Leu Ile
          35             40             45
Tyr Gly Val Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
          50             55             60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65             70             75             80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Asn Trp Tyr Thr
          85             90             95
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
          100             105

```

```

<210> SEQ ID NO 475
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 475

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cagagtatta ctcctac 18

```

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<210> SEQ ID NO 476
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 476

```

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Gln Ser Ile Thr Pro Tyr
 1             5

```

```

<210> SEQ ID NO 477
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

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<400> SEQUENCE: 477

```

```

ggtgtatcc 9

```

```

<210> SEQ ID NO 478
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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-continued

<220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 478

Gly Val Ser
 1

<210> SEQ ID NO 479
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 479

cagcagtatg acaactggta tact 24

<210> SEQ ID NO 480
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 480

Gln Gln Tyr Asp Asn Trp Tyr Thr
 1 5

<210> SEQ ID NO 481
 <211> LENGTH: 366
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 481

caggtgcagg tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgceg cctctggatt caccttcagt gactatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcaatt atatcatatg atggaagtaa taaatactat 180
 gcagactccg tgaagggccg attcaccgtg tccagagaca attccaagaa cactctgtat 240
 ctgcaattgg acagcctgag acctgaggac gcggctgtct tttactgtgc gagagagggg 300
 gcatttaact tagactacta cgccatggac gtctggggcc aagggacaac ggtcaccgtc 360
 tcctca 366

<210> SEQ ID NO 482
 <211> LENGTH: 122
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 482

Gln Val Gln Val Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Ile Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

-continued

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 488

Ala Arg Glu Gly Ala Phe Asn Leu Asp Tyr Tyr Ala Met Asp Val
 1 5 10 15

<210> SEQ ID NO 489

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 489

gccatccaga tgaccagtc tccatcctcc ctgtctgcct ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca ggacattaga aatgatttag gttggtatca gcagaaacca 120
 gggaaagccc ctaacctcct gatctatgct gcatccagtt taaaaagtgg ggtcccatca 180
 aggttcagcg gcagtgggtc tggcacagat ttcactctca ccatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtctacaa gattccaatt acccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa g 321

<210> SEQ ID NO 490

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 490

Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp
 20 25 30
 Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Ser Asn Tyr Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 491

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 491

caggacatta gaaatgat 18

<210> SEQ ID NO 492

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

-continued

 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 492

 Gln Asp Ile Arg Asn Asp
 1 5

<210> SEQ ID NO 493

<211> LENGTH: 9

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 493

gctgcatcc

9

<210> SEQ ID NO 494

<211> LENGTH: 3

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 494

 Ala Ala Ser
 1

<210> SEQ ID NO 495

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 495

ctacaagatt ccaattaccc gctcact

27

<210> SEQ ID NO 496

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 496

 Leu Gln Asp Ser Asn Tyr Pro Leu Thr
 1 5

<210> SEQ ID NO 497

<211> LENGTH: 670

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 497

 Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr Leu Asn Gly
 1 5 10 15

 Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr Leu Tyr Lys
 20 25 30

 Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
 35 40 45

 Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
 50 55 60

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Thr	Gly	Tyr	Val	Leu	Val	Ala	Met	Asn	Glu	Phe	Ser	Thr	Leu	Pro	Leu	65	70	75	80
Pro	Asn	Leu	Arg	Val	Val	Arg	Gly	Thr	Gln	Val	Tyr	Asp	Gly	Lys	Phe	85	90	95	
Ala	Ile	Phe	Val	Met	Leu	Asn	Tyr	Asn	Thr	Asn	Ser	Ser	His	Ala	Leu	100	105	110	
Arg	Gln	Leu	Arg	Leu	Thr	Gln	Leu	Thr	Glu	Ile	Leu	Ser	Gly	Gly	Val	115	120	125	
Tyr	Ile	Glu	Lys	Asn	Asp	Lys	Leu	Cys	His	Met	Asp	Thr	Ile	Asp	Trp	130	135	140	
Arg	Asp	Ile	Val	Arg	Asp	Arg	Asp	Ala	Glu	Ile	Val	Val	Lys	Asp	Asn	145	150	155	160
Gly	Arg	Ser	Cys	Pro	Pro	Cys	His	Glu	Val	Cys	Lys	Gly	Arg	Cys	Trp	165	170	175	
Gly	Pro	Gly	Ser	Glu	Asp	Cys	Gln	Thr	Leu	Thr	Lys	Thr	Ile	Cys	Ala	180	185	190	
Pro	Gln	Cys	Asn	Gly	His	Cys	Phe	Gly	Pro	Asn	Pro	Asn	Gln	Cys	Cys	195	200	205	
His	Asp	Glu	Cys	Ala	Gly	Gly	Cys	Ser	Gly	Pro	Gln	Asp	Thr	Asp	Cys	210	215	220	
Phe	Ala	Cys	Arg	His	Phe	Asn	Asp	Ser	Gly	Ala	Cys	Val	Pro	Arg	Cys	225	230	235	240
Pro	Gln	Pro	Leu	Val	Tyr	Asn	Lys	Leu	Thr	Phe	Gln	Leu	Glu	Pro	Asn	245	250	255	
Pro	His	Thr	Lys	Tyr	Gln	Tyr	Gly	Gly	Val	Cys	Val	Ala	Ser	Cys	Pro	260	265	270	
His	Asn	Phe	Val	Val	Asp	Gln	Thr	Ser	Cys	Val	Arg	Ala	Cys	Pro	Pro	275	280	285	
Asp	Lys	Met	Glu	Val	Asp	Lys	Asn	Gly	Leu	Lys	Met	Cys	Glu	Pro	Cys	290	295	300	
Gly	Gly	Leu	Cys	Pro	Lys	Ala	Cys	Glu	Gly	Thr	Gly	Ser	Gly	Ser	Arg	305	310	315	320
Phe	Gln	Thr	Val	Asp	Ser	Ser	Asn	Ile	Asp	Gly	Phe	Val	Asn	Cys	Thr	325	330	335	
Lys	Ile	Leu	Gly	Asn	Leu	Asp	Phe	Leu	Ile	Thr	Gly	Leu	Asn	Gly	Asp	340	345	350	
Pro	Trp	His	Lys	Ile	Pro	Ala	Leu	Asp	Pro	Glu	Lys	Leu	Asn	Val	Phe	355	360	365	
Arg	Thr	Val	Arg	Glu	Ile	Thr	Gly	Tyr	Leu	Asn	Ile	Gln	Ser	Trp	Pro	370	375	380	
Pro	His	Met	His	Asn	Phe	Ser	Val	Phe	Ser	Asn	Leu	Thr	Thr	Ile	Gly	385	390	395	400
Gly	Arg	Ser	Leu	Tyr	Asn	Arg	Gly	Phe	Ser	Leu	Leu	Ile	Met	Lys	Asn	405	410	415	
Leu	Asn	Val	Thr	Ser	Leu	Gly	Phe	Arg	Ser	Leu	Lys	Glu	Ile	Ser	Ala	420	425	430	
Gly	Arg	Ile	Tyr	Ile	Ser	Ala	Asn	Arg	Gln	Leu	Cys	Tyr	His	His	Ser	435	440	445	
Leu	Asn	Trp	Thr	Lys	Val	Leu	Arg	Gly	Pro	Thr	Glu	Glu	Arg	Leu	Asp	450	455	460	
Ile	Lys	His	Asn	Arg	Pro	Arg	Arg	Asp	Cys	Val	Ala	Glu	Gly	Lys	Val	465	470	475	480
Cys	Asp	Pro	Leu	Cys	Ser	Ser	Gly	Gly	Cys	Trp	Gly	Pro	Gly	Pro	Gly				

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485				490				495							
Gln	Cys	Leu	Ser	Cys	Arg	Asn	Tyr	Ser	Arg	Gly	Gly	Val	Cys	Val	Thr
			500					505					510		
His	Cys	Asn	Phe	Leu	Asn	Gly	Glu	Pro	Arg	Glu	Phe	Ala	His	Glu	Ala
		515					520					525			
Glu	Cys	Phe	Ser	Cys	His	Pro	Glu	Cys	Gln	Pro	Met	Glu	Gly	Thr	Ala
	530					535					540				
Thr	Cys	Asn	Gly	Ser	Gly	Ser	Asp	Thr	Cys	Ala	Gln	Cys	Ala	His	Phe
545					550					555					560
Arg	Asp	Gly	Pro	His	Cys	Val	Ser	Ser	Cys	Pro	His	Gly	Val	Leu	Gly
				565					570					575	
Ala	Lys	Gly	Pro	Ile	Tyr	Lys	Tyr	Pro	Asp	Val	Gln	Asn	Glu	Cys	Arg
			580					585					590		
Pro	Cys	His	Glu	Asn	Cys	Thr	Gln	Gly	Cys	Lys	Gly	Pro	Glu	Leu	Gln
		595					600					605			
Asp	Cys	Leu	Gly	Gln	Gly	Thr	Lys	Thr	His	Leu	Arg	Arg	Gly	Ser	Gly
	610					615					620				
Trp	Arg	Thr	Lys	Thr	His	Leu	Arg	Arg	Gly	Ser	Ala	Pro	Ser	Pro	Ser
625					630					635					640
Pro	Leu	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Gly	Gly	Glu	Gln
			645						650					655	
Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	His	His	His	His	His	His	His	His
			660					665						670	

<210> SEQ ID NO 498

<211> LENGTH: 840

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 498

Ser	Glu	Val	Gly	Asn	Ser	Gln	Ala	Val	Cys	Pro	Gly	Thr	Leu	Asn	Gly
1				5					10					15	
Leu	Ser	Val	Thr	Gly	Asp	Ala	Glu	Asn	Gln	Tyr	Gln	Thr	Leu	Tyr	Lys
			20					25					30		
Leu	Tyr	Glu	Arg	Cys	Glu	Val	Val	Met	Gly	Asn	Leu	Glu	Ile	Val	Leu
		35					40					45			
Thr	Gly	His	Asn	Ala	Asp	Leu	Ser	Phe	Leu	Gln	Trp	Ile	Arg	Glu	Val
	50					55					60				
Thr	Gly	Tyr	Val	Leu	Val	Ala	Met	Asn	Glu	Phe	Ser	Thr	Leu	Pro	Leu
65					70					75					80
Pro	Asn	Leu	Arg	Val	Val	Arg	Gly	Thr	Gln	Val	Tyr	Asp	Gly	Lys	Phe
			85						90					95	
Ala	Ile	Phe	Val	Met	Leu	Asn	Tyr	Asn	Thr	Asn	Ser	Ser	His	Ala	Leu
			100					105					110		
Arg	Gln	Leu	Arg	Leu	Thr	Gln	Leu	Thr	Glu	Ile	Leu	Ser	Gly	Gly	Val
		115					120						125		
Tyr	Ile	Glu	Lys	Asn	Asp	Lys	Leu	Cys	His	Met	Asp	Thr	Ile	Asp	Trp
	130					135					140				
Arg	Asp	Ile	Val	Arg	Asp	Arg	Asp	Ala	Glu	Ile	Val	Val	Lys	Asp	Asn
145					150					155					160
Gly	Arg	Ser	Cys	Pro	Pro	Cys	His	Glu	Val	Cys	Lys	Gly	Arg	Cys	Trp
			165						170					175	
Gly	Pro	Gly	Ser	Glu	Asp	Cys	Gln	Thr	Leu	Thr	Lys	Thr	Ile	Cys	Ala

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180				185				190							
Pro	Gln	Cys	Asn	Gly	His	Cys	Phe	Gly	Pro	Asn	Pro	Asn	Gln	Cys	Cys
		195					200					205			
His	Asp	Glu	Cys	Ala	Gly	Gly	Cys	Ser	Gly	Pro	Gln	Asp	Thr	Asp	Cys
	210					215					220				
Phe	Ala	Cys	Arg	His	Phe	Asn	Asp	Ser	Gly	Ala	Cys	Val	Pro	Arg	Cys
	225				230					235					240
Pro	Gln	Pro	Leu	Val	Tyr	Asn	Lys	Leu	Thr	Phe	Gln	Leu	Glu	Pro	Asn
				245					250					255	
Pro	His	Thr	Lys	Tyr	Gln	Tyr	Gly	Gly	Val	Cys	Val	Ala	Ser	Cys	Pro
			260					265						270	
His	Asn	Phe	Val	Val	Asp	Gln	Thr	Ser	Cys	Val	Arg	Ala	Cys	Pro	Pro
		275					280					285			
Asp	Lys	Met	Glu	Val	Asp	Lys	Asn	Gly	Leu	Lys	Met	Cys	Glu	Pro	Cys
	290					295					300				
Gly	Gly	Leu	Cys	Pro	Lys	Ala	Cys	Glu	Gly	Thr	Gly	Ser	Gly	Ser	Arg
	305				310					315					320
Phe	Gln	Thr	Val	Asp	Ser	Ser	Asn	Ile	Asp	Gly	Phe	Val	Asn	Cys	Thr
				325					330					335	
Lys	Ile	Leu	Gly	Asn	Leu	Asp	Phe	Leu	Ile	Thr	Gly	Leu	Asn	Gly	Asp
			340					345						350	
Pro	Trp	His	Lys	Ile	Pro	Ala	Leu	Asp	Pro	Glu	Lys	Leu	Asn	Val	Phe
		355					360						365		
Arg	Thr	Val	Arg	Glu	Ile	Thr	Gly	Tyr	Leu	Asn	Ile	Gln	Ser	Trp	Pro
	370					375					380				
Pro	His	Met	His	Asn	Phe	Ser	Val	Phe	Ser	Asn	Leu	Thr	Thr	Ile	Gly
				390						395					400
Gly	Arg	Ser	Leu	Tyr	Asn	Arg	Gly	Phe	Ser	Leu	Leu	Ile	Met	Lys	Asn
				405					410					415	
Leu	Asn	Val	Thr	Ser	Leu	Gly	Phe	Arg	Ser	Leu	Lys	Glu	Ile	Ser	Ala
			420					425					430		
Gly	Arg	Ile	Tyr	Ile	Ser	Ala	Asn	Arg	Gln	Leu	Cys	Tyr	His	His	Ser
		435					440					445			
Leu	Asn	Trp	Thr	Lys	Val	Leu	Arg	Gly	Pro	Thr	Glu	Glu	Arg	Leu	Asp
	450					455					460				
Ile	Lys	His	Asn	Arg	Pro	Arg	Arg	Asp	Cys	Val	Ala	Glu	Gly	Lys	Val
	465				470					475					480
Cys	Asp	Pro	Leu	Cys	Ser	Ser	Gly	Gly	Cys	Trp	Gly	Pro	Gly	Pro	Gly
				485					490					495	
Gln	Cys	Leu	Ser	Cys	Arg	Asn	Tyr	Ser	Arg	Gly	Gly	Val	Cys	Val	Thr
			500					505					510		
His	Cys	Asn	Phe	Leu	Asn	Gly	Glu	Pro	Arg	Glu	Phe	Ala	His	Glu	Ala
		515					520					525			
Glu	Cys	Phe	Ser	Cys	His	Pro	Glu	Cys	Gln	Pro	Met	Glu	Gly	Thr	Ala
		530				535					540				
Thr	Cys	Asn	Gly	Ser	Gly	Ser	Asp	Thr	Cys	Ala	Gln	Cys	Ala	His	Phe
	545				550					555					560
Arg	Asp	Gly	Pro	His	Cys	Val	Ser	Ser	Cys	Pro	His	Gly	Val	Leu	Gly
				565					570					575	
Ala	Lys	Gly	Pro	Ile	Tyr	Lys	Tyr	Pro	Asp	Val	Gln	Asn	Glu	Cys	Arg
			580					585					590		
Pro	Cys	His	Glu	Asn	Cys	Thr	Gln	Gly	Cys	Lys	Gly	Pro	Glu	Leu	Gln
		595					600					605			

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Asp Cys Leu Gly Gln Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 610 615 620
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 625 630 635 640
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 645 650 655
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 660 665 670
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 675 680 685
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 690 695 700
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 705 710 715 720
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 725 730 735
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 740 745 750
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 755 760 765
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 770 775 780
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 785 790 795 800
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 805 810 815
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 820 825 830
 Ser Leu Ser Leu Ser Pro Gly Lys
 835 840

<210> SEQ ID NO 499
 <211> LENGTH: 846
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 499

Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr Leu Asn Gly
 1 5 10 15
 Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr Leu Tyr Lys
 20 25 30
 Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
 35 40 45
 Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
 50 55 60
 Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr Leu Pro Leu
 65 70 75 80
 Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp Gly Lys Phe
 85 90 95
 Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser His Ala Leu
 100 105 110
 Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser Gly Gly Val
 115 120 125

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Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr Ile Asp Trp
 130 135 140

Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val Lys Asp Asn
 145 150 155 160

Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly Arg Cys Trp
 165 170 175

Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr Ile Cys Ala
 180 185 190

Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn Gln Cys Cys
 195 200 205

His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp Thr Asp Cys
 210 215 220

Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val Pro Arg Cys
 225 230 235 240

Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu Glu Pro Asn
 245 250 255

Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala Ser Cys Pro
 260 265 270

His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala Cys Pro Pro
 275 280 285

Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys Glu Pro Cys
 290 295 300

Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser Gly Ser Arg
 305 310 315 320

Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val Asn Cys Thr
 325 330 335

Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu Asn Gly Asp
 340 345 350

Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu Asn Val Phe
 355 360 365

Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln Ser Trp Pro
 370 375 380

Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr Thr Ile Gly
 385 390 395 400

Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile Met Lys Asn
 405 410 415

Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu Ile Ser Ala
 420 425 430

Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr His His Ser
 435 440 445

Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu Arg Leu Asp
 450 455 460

Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu Gly Lys Val
 465 470 475 480

Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro Gly Pro Gly
 485 490 495

Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val Cys Val Thr
 500 505 510

His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala His Glu Ala
 515 520 525

Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu Gly Thr Ala
 530 535 540

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Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys Ala His Phe
 545 550 555 560
 Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly Val Leu Gly
 565 570 575
 Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn Glu Cys Arg
 580 585 590
 Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro Glu Leu Gln
 595 600 605
 Asp Cys Leu Gly Gln Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro
 610 615 620
 Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe
 625 630 635 640
 Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro
 645 650 655
 Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val
 660 665 670
 Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr
 675 680 685
 Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala
 690 695 700
 Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys
 705 710 715 720
 Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser
 725 730 735
 Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro
 740 745 750
 Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val
 755 760 765
 Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly
 770 775 780
 Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp
 785 790 795 800
 Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp
 805 810 815
 Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His
 820 825 830
 Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
 835 840 845

<210> SEQ ID NO 500
 <211> LENGTH: 227
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <400> SEQUENCE: 500

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1 5 10 15
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 20 25 30
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 35 40 45
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 50 55 60

-continued

His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
65					70					75					80
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
			85						90					95	
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
			100					105					110		
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
		115					120					125			
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
	130					135					140				
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
145					150					155					160
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
				165					170					175	
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
			180					185					190		
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
		195					200					205			
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
	210					215					220				
Pro	Gly	Lys													
225															

What is claimed is:

1. A method for extending or prolonging the survival of a subject afflicted with a cancer expressing ErbB3 and one or more of EGFR, HER2, ErbB4, EGFRvIII, VEGF and DLL4, the method comprising administering to the subject (i) a therapeutically effective amount of an anti-ErbB3 antibody or an antigen binding fragment thereof and (ii) a therapeutically effective amount of a second component selected from an anti-EGFR antibody or an antigen-binding fragment thereof, a small molecule inhibitor of EGFR activity, an anti-HER2 antibody or an antigen-binding fragment thereof, an anti-ErbB4 antibody or an antigen-binding fragment thereof, an anti-EGFRvIII antibody or an antigen-binding fragment thereof, a VEGF antagonist, an anti-VEGF antibody or an antigen-binding fragment thereof, a small molecule kinase inhibitor of VEGF receptor, or an anti-DLL4 antibody or an antigen-binding fragment thereof;

wherein the anti-ErbB3 antibody or an antigen-binding fragment thereof comprises three heavy chain complementarity determining regions (HCDR1, HCDR2, and HCDR3) comprising the amino acid sequence of SEQ ID NOs: 324, 326 and 328, respectively, and three light chain complementarity determining regions (LCDR1, LCDR2, and LCDR3) comprising the amino acid sequence of SEQ ID NOs: 332, 334 and 336, respectively.

2. The method of claim 1, wherein the anti-ErbB3 antibody or antigen-binding fragment thereof comprises a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO:322, and a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO:330.

30

3. The method of claim 1, wherein the anti-EGFR antibody is selected from cetuximab, panitumumab, an antigen-binding fragment of cetuximab or an antigen-binding fragment of panitumumab.

35 4. The method of claim 1, wherein the small molecule inhibitor of EGFR activity is selected from erlotinib or gefitinib.

5. The method of claim 1, wherein the VEGF antagonist is a VEGF-Trap.

40 6. The method of claim 1, wherein the anti-VEGF antibody is selected from bevacizumab or an antigen-binding fragment of bevacizumab.

7. The method of claim 1, wherein the small molecule kinase inhibitor of VEGF receptor is selected from sunitinib, sorafenib, or pazopanib.

45 8. The method of claim 1, wherein the anti-ErbB3 antibody or antigen-binding fragment thereof and the second component are administered to the subject in separate dosage forms.

50 9. The method of claim 8, wherein the separate dosage forms are administered to the subject simultaneously.

10. The method of claim 8, wherein the separate dosage forms are administered to the subject sequentially.

55 11. The method of claim 1, wherein the anti-ErbB3 antibody or antigen-binding fragment thereof and the second component are administered to the subject in a single dosage form.

60 12. The method of claim 2, wherein the anti-ErbB3 antibody or antigen-binding fragment thereof and the second component are administered to the subject in separate dosage forms.

* * * * *